

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2004, 21:40:18 ; Search time 5813 Seconds

(without alignments)
10766.788 Million cell updates/sec

Title: US-09-868-744B-1

Perfect score: 1444
Sequence: 1 atcatgattcctaatacatc.....gtactggaatgtagatcc 1444Scoring table: IDENTITY NUC
Gapop 10_0, Gapexc 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
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41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1442	99.9	1444	6	AX026532
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3	1341.8	92.9	6385	6	AX463618
4	1341.4	92.9	4526	6	AX463617
5	1306.2	90.5	11127	6	AX392814
6	1298.4	89.9	3450	6	AX463620
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ALIGNMENTS

RESULT 1
AX026532
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DEFINITION Sequence 1 from Patent WO0037661.
ACCESSION AX026532
VERSION AX026532.1 GI.10187719
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
Pettig, J.H., Schepers, F.M. and van Dun Cornelis, M.P.
AUTHORS
TITLE Genetic modification of compositae

'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Graal (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/Graal-1.3/>), GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and SplicePredictor (Volker Brendel, Stanford University, <http://gremlin.zool.iastate.edu/cgi-bin/sp.cgi>). Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is K249 and the 3' clone is MCB22.

FEATURES

SOURCE

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CDS

CDS

CDS

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CDS

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ACCESSION	AX463618				
VERSION	AX463618.1	GI:21886378			
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ORGANISM	REFERENCE				
	AUTHORS				
	TITLE				
	Meagher,R.B. and Li,Y.				
	Metal resistant plants and phytoremediation of environmental				
	contamination				
	Patent: WO 0248335-A 15 20-JUN-2002;				
JOURNAL					

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RESULT 5
AX392814
LOCUS AX392814 11127 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 17 from Patent WO0215701.
ACCESSION AX392814
VERSION AX392814.1 GI:19700916
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Carotzi,N.B., Rabe,S.M., Miles,P.J., Warren,G.W. and de Haan,P.T.
TITLE Novel insecticidal toxins derived from Bacillus thuringiensis
JOURNAL insecticidal crystal proteins
Patent: WO 0215701-A 17 28-FEB-2002;
Syngenta Participations AG (CH)
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3859..5030
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5052..6271
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Query Match 90.5%; Score 1306.2; DB 6; Length 11127;
Best Local Similarity 98.8%; Pred.No. 1.2e-273;
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QY 1377 AAAAA 1381
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QY 1470 AAAAA 1474
Db |||||
RESULT 6
AX463620
LOCUS AX463620
DEFINITION Sequence 17 from Patent WO0248335.
ACCESSION AX463620
VERSION AX463620.1 GI:21886380
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Meagher,R.B. and Li,Y.
TITLE Metal resistant plants and phyto remediation of environmental
JOURNAL contamination
Patent: WO 0248335-A 17 20-JUN-2002;
UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC. (US)
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Best Local Similarity 98.1%; Pred. No. 6.7e-272;
Matches 1376; Conservative 0; Mismatches 18; Indels 8; Gaps 6;
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AX463619
LOCUS AX463619 3408 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 16 from Patent WO0248335.
ACCESSION AX463619
VERSION AX463619.1 GI:21886379
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
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REFERENCE
Meagher R.B. and Li, Y.
Metal resistant plants and phytoremediation of environmental
contamination
Patent: WO 0248335-A 16 20-JUN-2002;
JOURNAL UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.. (US)

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Best Local Similarity 98.5%; Pred. No. 1.1e-271;
Matches 1372; Conservative 0; Mismatches 13; Indels 8; Gaps 6;

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RESULT 8
AX463621
LOCUS 2857 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 18 from Patent WO0248335.
ACCESSION AX463621
VERSION AX463621.1 GI:21886381
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Meagher, R. B. and Li, Y.
TITLE Metal resistant plants and phyto remediation of environmental
JOURNAL contamination
Patent: WO 0248335-A 18 20-JUN-2002;
UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC. (US)
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Best Local Similarity 98.6%; Pred. No. 1.4e-271;
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Qy 1017 GGATCTGTGAACCTCCCACTAAATCTTTTGGTTTACTAGAACTGATCTAAAGTTGACCGAT 1076
Db 1026 GGATCTGTGAACCTCCCACTAAATCTTTTGGTTTACTAGAACTGATCTAAAGTTGACCGAT 1085
Qy 1077 CAGTACCTCGATATAGTACACGAATTTGGCTTGACCTTGATGAGAGATCCATGTTTC 1136
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Qy 1137 ATGTACCTCGGAATGATTTGTATATGTAATGTAATCTGAACTCTGAACTGTTGAAGTTAGATT 1196
Db 1146 ATGTACCTCGGAATGATTTGTATATGTAATGTAATCTGAACTCTGAACTGTTGAAGTTAGATT 1205
Qy 1197 GAATCTGAACCTGTAATGTTAGATTAATCTGAACCTGTTTAA-GTTAGATGAAGTT 1255
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Db      1206 GAATCTGAACACTGCTCAATGTTAGATTGAATCTGAACACTGTTTAAAGTTAGATGAAGTT 1265
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Db      1266 TGTGATAGATCTTCGAACACTTAGGATTTGTAGTGTGTAACGTTGAACAGAAAGCTAT 1325
QY      1316 TTTCTGATTCATCAGGGTTTATTCAGCTGATTAAGCTTTTGTGTTTGTGCTGACCTCA 1375
Db      1326 TTTCTGATTCATCAGGGTTTATTCAGCTGATTAAGCTTTTGTGTTTGTGCTGACCTCA 1385
QY      1376 TAAAAATGGC 1386
Db      1386 TAAACCATGGC 1396

RESULT 9
LOCUS   ATU41998
DEFINITION Arabidopsis thaliana actin 2 (ACT2) gene, complete cds.
ACCESSION U41998
VERSION   U41998.1 GI:1669386
KEYWORDS
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 3172)
AUTHORS  An, Y.-Q., McDowell, J.M., Huang, S., McKinney, E.C., Chambliss, S. and
Meadner, R.B.
TITLE    Strong, constitutive expression of the Arabidopsis ACT2/ACT8 actin
subclass in vegetative tissues
JOURNAL  Plant J. 10 (1), 107-121 (1996)
MEDLINE  96314863
PUBMED  8759881
REFERENCE 2 (bases 1 to 3172)
AUTHORS  An, Y.-Q.
TITLE    Direct Submission
JOURNAL  Submitted (05-DEC-1995) Yong-Qiang An, Department of Genetics,
University of Georgia, Athens, GA 30602, USA
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VSHVTPEYFSLPHAILRLDLAQRDLTLMKILITERGYMFTTAEREIVRDIKEL
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ORIGIN
Query Match 85.5%; Score 1234.2; DB 8; Length 3172;
Best Local Similarity 99.1%; Pred. NO. 6.1e-258;
Matches 1263; Conservative 0; Mismatches 8; Indels 4; Gaps 2;

QY      164 CAACATATTTTATGATGCAAGAGTCAGCATATGATATGATTCAGATCGTTTTCAC 223
Db      1 CAACATATTTTATGATGCAAGAGTCAGCATATGATATGATTCAGATCGTTTTCAC 60

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QY      224 GATTCGGATGTAGTAGCCATATTTTAATGTACATCTAATCGTGAATAGTGATG 283
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QY      284 ATCAACATCTGATCTTATTTGTATTAATCCATAACACATCATGAAGACACTTCTT 343
Db      121 ATGAACATCTGATCTTATTTGTATTAATCCATAACACATCATGAAGACACTTCTT 180
QY      344 TCAGGCTCTGAATTAATTAATGATCAATTTCTAATAGAAAACGAATTAATTAAGTGAAT 403
Db      181 TCACGCTCTGAATTAATTAATGATCAATTTCTAATAGAAAACGAATTAATTAAGTGAAT 240
QY      404 TGTATGAATCTAATTTGAACAGCCACACGACGAGGACTAAAGTTCCTGAGTACT 463
Db      241 TGTATGAATCTAATTTGAACAGCCACACGACGAGGACTAAAGTTCCTGAGTACT 300
QY      464 CGGTTTAACTTAACACTTAAAAAAACGAGCTGTCAATGAACAACGCGATCGAGAGTGC 523
Db      301 CGGTTTAACTTAACACTTAAAAAAACGAGCTGTCAATGAACAACGCGATCGAGAGTGC 360
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Db      601 TCTCGTGTCTCTCTCACTTCTCATCAGCCGTTTGAATCTCCGCGACTTCAGCAGAGAG 660
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Db      661 AACAGAGAGAAAGACTAAGAGAGAAAGTAAGAGATAATCCAGAGATTCATTCCTCGTTT 720
QY      883 TGAATCTCTCAATCTCATCTCTTCTTCCGCTCTTCTTCCAGAGTAAAGAGACTT 942
Db      721 TGAATCTCTCAATCTCA---TCTTCTCCGCTCTTCTTCCAGAGTAAAGAGACTT 777
QY      943 TCTGGATCTACTTTTATTTGCTGATCTCGATCTTGTGTTTCTCAATTCCTTGAGATCTGG 1002
Db      778 TCTGGATCTACTTTTATTTGCTGATCTCGATCTTGTGTTTCTCAATTCCTTGAGATCTGG 837
QY      1003 AATTGCTTAAATTTGGATCTGTGAACCTCCACTAAATCTTTTGGTTTACTAGATTCGAT 1062
Db      838 AATTGCTTAAATTTGGATCTGTGAACCTCCACTAAATCTTTTGGTTTACTAGATTCGAT 897
QY      1063 CTAAGTTACCGATCAGTTAGTCTCGATTTATAGTACACAGAAATTTGGCTTACGCTTGG 1122
Db      898 CTAAGTTACCGATCAGTTAGTCTCGATTTATAGTACACAGAAATTTGGCTTACGCTTGG 957
QY      1123 AGAGATCCAATGCTCATGTTTACCTGGAAAAGTATTTGATGTGAATGAATCTGAATCT 1182
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QY      1243 GTTAGATGAAGTTTGTGTATAGATTTCTTCGAAACCTTAGGATTTGTAGTCTGCTGTTG 1302
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QY 1303 AACAGAACTATTTCTGATTCATCAATCAGGGTTTATTTGACTGTATTAATGAATCTTTTGG 1362
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Db 1198 TGTTCAGCTCATATAAAATGCTCAGGCTGAGCATTAACCAATCGTGTGTGACAA 1257
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Db 1258 TGGTACCGGTATGGT 1272
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RESULT 10
AX461227 1217 bp DNA linear PAT 08-JUL-2002
LOCUS
DEFINITION Sequence 156 from Patent WO0198480.
ACCESSION AX461227
VERSION AX461227.1 GI:21726435
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1
REFERENCE Budworth, P., Brown, D., Chang, H.S., Zhu, T., Han, B., Wang, X. and
AUTHORS Cooper, B.
TITLE Promoters for regulation of plant gene expression
JOURNAL Patent: WO 0198480-A 156 27-DEC-2001;
Syngenta Participations AG (CH)
FEATURES
Location/Qualifiers
Source 1..1217
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ORIGIN
Query Match 82.0%; Score 1184; DB 6; Length 1217;
Best Local Similarity 99.3%; Pred. No. 5.6e-247;
Matches 1211; Conservative 0; Mismatches 5; Indels 4; Gaps 2;

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QY 224 GAGTTCGGATGTAGTAGTACCCATTTATTAATGTACATCTAATCGTGAATAGTATATG 283
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QY 284 ATGAACATTTGTATCTTATTTGTATAAATATCCATAAACAATCAATGAAGACATTTCTT 343
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RESULT 11
AR236191 1219 bp DNA linear PAT 20-DEC-2002
LOCUS
DEFINITION Sequence 9 from patent US 6462258.
ACCESSION AR236191
VERSION AR236191.1 GI:27280000
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1. (bases 1 to 1219)
AUTHORS Fincher, K.L. and Wilkinson, J.Q.
TITLE Plant expression constructs
JOURNAL Patent: US 6462258-A 9 08-OCT-2002;
FEATURES
Location/Qualifiers
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/organism="unknown"
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ORIGIN

Query Match 81.4%; Score 1174.8; DB 6; Length 1219;
Best Local Similarity 98.7%; Pred. No. 5.6e-245;
Matches 1206; Conservative 0; Mismatches 12; Indels 4; Gaps 2;

QY 164 CAACTATTTTATGATGCAAGAGTCAGCATATGTATAATTTGATTCAGAACTGGTTTGCAC 223
DB 1 CAACTATTTTATGATGCAAGAGTCAGCATATGTATAATTTGATTCAGAACTGGTTTGCAC 60

QY 224 GAGTTCGGATGTAGTAGCCATTATTTAATGTACATACATTAATTCGATGATGATG 293
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DB 481 TGTGTCGAAATGATTCGTCTGTCGATTTTAAATTTTAAAGGCGCGAAATAA 540

QY 703 AGTTGTAAGAGATAAAGCCGCTATATAAATTCATATTTTCTCCCGCTTGAATG 762
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QY 823 AACAGGAGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGAGATTCATTTCCGGTTT 882
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QY 943 TCTGGATCTACTTTATTTGTCGATCTCGATCTTGTCTTCTCAATTTCTTGGATCTGG 1002
DB 778 TCTGGATCTACTTTATTTGTCGATCTCGATCTTGTCTTCTCAATTTCTTGGATCTGG 837

QY 1003 AATTCCGTTTAAATTTGGATCTGTGAACCTCCAATAATCTTTTGGTTTATAGAAATCGAT 1062
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QY 1063 CTAAGTTGACCGATCAGTTAGCTCGATTTATAGCTACCAAGTTTGGCTTACCGCTTGGG 1122
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QY 1183 GTTGAAGTTAGATTAATCTGAACACTCTCAATGTTAGATTGAATCTGAACACTGTTTAA 1242
DB 1018 GTTGAAGTTAGATTAATCTGAACACTCTCAATGTTAGATTGAATCTGAACACTGTTTAA 1077

QY 1243 GTTGAATGAAGTTTGTGTATAGATTTCTTCGAAACCTTAGGATTTGTAGTCTGACGTTG 1302
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QY 1363 TGTTCGAGCTCATAAAAAATG 1384
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RESULT 12
AR438153
LOCUS AR438153 1219 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 9 from patent US 6660911.
ACCESSION AR438153
VERSION AR438153.1 GI:40204655
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1219)
AUTHORS Fincher, K.L., Flasinger, S. and Wilkinson, J.O.
TITLE Plant expression constructs
JOURNAL Patent: US 6660911-A 9 09-DEC-2003;
FEATURES Location/Qualifiers
source 1..1219
/organism="unknown"
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ORIGIN
Query Match 81.4%; Score 1174.8; DB 6; Length 1219;
Best Local Similarity 98.7%; Pred. No. 5.6e-245;
Matches 1206; Conservative 0; Mismatches 12; Indels 4; Gaps 2;

QY 164 CAACTATTTTATGATGCAAGAGTCAGCATATGTATAATTTGATTCAGAACTGGTTTGCAC 223
DB 1 CAACTATTTTATGATGCAAGAGTCAGCATATGTATAATTTGATTCAGAACTGGTTTGCAC 60

QY 224 GAGTTCGGATGTAGTAGCCATTATTTAATGTACATACATTAATTCGATGATGATG 283
DB 61 GAGTTCGGATGTAGTAGCCATTATTTAATGTACATACATTAATTCGATGATGATG 120

QY 284 ATGAACAATCTATCTTATTTGATTAATAATCCATAAACAACATGATGAAGACACTTTCCT 343
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QY 344 TCAGGCTCTGAATTAATTAATGATCAATTTCTAATAGAAAAGAAATTAATTCGTTGAAT 403
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QY 404 TGTATGAATCTAATTTGACAGCCCAACCGACGAGGACTAAGCTTGCCTGGATTCGACT 463
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DB 301 CGGTTTAAAGTTTAAACAGGAGGAAA-GCTGTCTGACAGCGAGTCAAGTTATCTTTACC 360

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QY 1363 TGTTTGCAGCTCATAAAAATG 1384
Db 1198 TGTTTGCAGCTCATCAATG 1219
RESULT 14
AR236212
LOCUS 1742 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 30 from patent US 6462258.
ACCESSION AR236212
VERSION AR236212.1 GI:27280021
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1742)
AUTHORS Finch, K.L. and Wilkinson, J.Q.
TITLE Plant expression constructs
JOURNAL Patent: US 6462258-A 30 08-OCT-2002;
FEATURES
Location/Qualifiers
1. 1742
/organism="unknown"
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ORIGIN
Query Match 81.3%; Score 1174; DB 6; Length 1742;
Best Local Similarity 99.3%; Pred. No. 8e-245;
Matches 1201; Conservative 0; Mismatches 5; Indels 4; Gaps 2;
QY 164 CAACATTTTATGATGCAAGAGTCAGCATATGATATTAATTCAGATCGTTTGCAC 223
Db 533 CAACATTTTATGATGCAAGAGTCAGCATATGATATTAATTCAGATCGTTTGCAC 592
QY 224 GAGTTCGGATGTAGTAGCCATTATTAATGTACATACATAATCGTGAATAGTGATG 283
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Db 653 ATGAACATGTATCTTATGTATTAATATCCATTAACACATCATGAAGACACTTCTT 712
QY 344 TCAGGCTGTAATTAATGATACAAATCTTAATAGAAACGAATTAATGATGAT 403
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QY 404 TGATGAAATCTTAATTAAGAACCAACCAACGACGAGCTAATCGTCCCTGGATTGACT 463
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Db 833 CGGTTAAGTTAAACCACTAAAAAAGCGAGCTGTATGTAACCGGATCGAGAGGTC 892
QY 524 ACAGTCAATGAGCCATCAAGCAAGAAAGACTAATCCAGGGGTGAGATGATTAATGTT 583
Db 893 ACAGTCAATGAGCCATCAAGCAAGAAAGACTAATCCAGGGGTGAGATGATTAATGTT 952

QY 584 TAAATATTAGTTTAAACAGGAGAAA-GCTGTCTGACAGCAGGTCAGCTTATCTTTACC 642
Db 953 TAAATATTAGTTTAAACAGGAGAAAAGCTGTCTGACAGCAGGTCAGCTTATCTTTACC 1012
QY 643 TGTGTCGAAATGATTCGTGTCGTGATTTAATTTATTTTGAAGCCGAAATAA 702
Db 1013 TGTGTCGAAATGATTCGTGTCGTGATTTAATTTATTTTGAAGCCGAAATAA 1072
QY 703 AGTTGTAGAGATAAACCAGCCCTATATAAATCATATATTTCTCCCGCTTTGAATG 762
Db 1073 AGTTGTAGAGATAAACCAGCCCTATATAAATCATATATTTCTCCCGCTTTGAATG 1132
QY 763 TCTCGTGTCTCTCTCATCTTTCATCAGCCGTTTGAATCTCCGCGACTTGACAGAGAAG 822
Db 1133 TCTCGTGTCTCTCTCATCTTTCATCAGCCGTTTGAATCTCCGCGACTTGACAGAGAAG 1192
QY 823 AACAGGAAGAAGCTAAGAGAGAAAGTAAGAGATTAATCCAGGAGATTCATCTCCGTT 882
Db 1193 AACAGGAAGAAGCTAAGAGAGAAAGTAAGAGATTAATCCAGGAGATTCATCTCCGTT 1252
QY 883 TGAATCTTCTCAATCTCATCTTCTTCTCCGCTCTTCTTCCAGGTAATAGGAATCT 942
Db 1253 TGAATCTTCTCAATCTCA---TCTTCTCCGCTCTTCTTCCAGGTAATAGGAATCT 1309
QY 943 TCTGGATCTACTTTATTTGCTGATCTCGATCTTTGTTTCTCAATTTCTCTTGAGATCTCG 1002
Db 1310 TCTGGATCTACTTTATTTGCTGATCTCGATCTTTGTTTCTCAATTTCTCTTGAGATCTCG 1369
QY 1003 AATCGTTTAAATTTGATCTGTAACCTCCACTAAATCTTTGTTTCTACTAGATCGAT 1062
Db 1370 AATCGTTTAAATTTGATCTGTAACCTCCACTAAATCTTTGTTTCTACTAGATCGAT 1429
QY 1063 CTAAGTTGACCGATCAGTAGCTCGATTTAGCTTACCGAATTTGGCTTGACCTTGATGG 1122
Db 1430 CTAAGTTGACCGATCAGTAGCTCGATTTAGCTTACCGAATTTGGCTTGACCTTGATGG 1489
QY 1123 AGAGATCCATGTTTCACTACCTGGAAATGATTTGATATGTAATGAAATCTGAAT 1182
Db 1490 AGAGATCCATGTTTCACTACCTGGAAATGATTTGATATGTAATGAAATCTGAAT 1549
QY 1183 GTTGAAGTTAGATTGAATCTGAACACTGTGAATGTTAGATTGAATCTGAACACTGTTAA 1242
Db 1550 GTTGAAGTTAGATTGAATCTGAACACTGTGAATGTTAGATTGAATCTGAACACTGTTAA 1609
QY 1243 GTTGAAGTTAGATTGTTGATAGATCTTTCGAAACCTTAGGATTTCTAGTGTGATGTTG 1302
Db 1610 GTTGAAGTTAGATTGTTGATAGATCTTTCGAAACCTTAGGATTTCTAGTGTGATGTTG 1669
QY 1303 AACAGAAAGCTATTTCTGATCAATCAGGTTTATTTAGCTGATTTGAACTCTTTTGTG 1362
Db 1670 AACAGAAAGCTATTTCTGATCAATCAGGTTTATTTAGCTGATTTGAACTCTTTTGTG 1729
QY 1363 TGTTTGCAGC 1372
Db 1730 TGTTTGCAGC 1739
RESULT 15
AR438174
LOCUS 1742 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 30 from patent US 6660911.
ACCESSION AR438174
VERSION AR438174.1 GI:40204676
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1742)
AUTHORS Finch, K.L., Plasinski, S. and Wilkinson, J.Q.
TITLE Plant expression constructs
JOURNAL Patent: US 6660911-A 30 09-DEC-2003;
FEATURES
Location/Qualifiers
1. 1742
source

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OM nucleic - nucleic search, using sw model

Run on: March 14, 2004, 20:42:58 ; Search time 673 Seconds

(without alignments)
9115.005 Million cell updates/sec

Title: US-09-868-744B-1

Perfect score: 1444

Sequence: 1 attagatctcaatacatt.....gtactgaagttagatcc 1444

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapept 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq 29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1442	99.9	1444	3	AAA61367 Arabidops
2	1341.8	92.9	6385	6	Abk89341 Plasmid p
3	1341.4	92.9	4526	6	Abk89340 Plasmid p
4	1306.2	90.5	11127	6	Aad36967 Arabidops
5	1298.4	89.9	3450	6	Abk89343 Plasmid p
6	1297.4	89.8	3408	6	Abk89342 Plasmid p
7	1297	89.8	2857	6	Abk89344 Plasmid p
8	1174.8	81.4	1219	4	Aad09791 Arabidops
9	1174	81.3	1742	4	Aad09812 Chimeric
10	1114.6	77.2	12304	7	Abv75876 Luciferas
11	1104.6	76.5	1259	6	Abk52080 Modified
12	1078.8	74.7	15676	3	Aad01288 Arabidops
13	1078.8	74.7	17111	3	Aad01289 Arabidops
14	1078.8	74.7	17116	3	Aad01290 Arabidops
15	1053	72.9	1202	6	Abk52077 Modified
16	1001.8	69.4	1342	6	Abk52081 Modified
17	950.2	65.8	1285	6	Abk52078 Modified
18	784.4	54.3	910	6	Abk52079 Modified
19	732.8	50.7	853	6	Abk52076 Modified
20	579	40.1	1228	6	Abk53111 Transgene
21	475.8	33.0	11461	4	Aad02175 Plasmid p
22	474.8	32.9	12766	4	Aad02174 Plasmid p
23	163	11.3	1486	3	Aac33486 Arabidops

C	24	116.4	8.1	1228	6	ABSS3111	Abss3111 Transgene
	25	110	7.6	573	7	ABX56906	Abx56906 Arabidops
	26	94	6.5	94	6	ABK52089	Abk52089 Synthetic
	27	84.4	5.8	97	6	ABK52087	Abk52087 Synthetic
	28	79	5.5	79	6	ABK52084	Abk52084 Synthetic
	29	77.4	5.4	79	6	ABK52092	Abk52092 Synthetic
	30	76	5.3	2000	6	ABZ15497	Abz15497 Arabidops
	31	75.4	5.2	1271	4	AAD09792	Aad09792 Arabidops
	32	73.8	5.1	1800	4	AAD09811	Aad09811 Chimeric
	33	65.4	4.5	67	6	ABK52085	Abk52085 Synthetic
	34	65.4	4.5	74	6	ABK52082	Abk52082 Synthetic
	35	63.4	4.4	77	6	ABK52083	Abk52083 Synthetic
C	36	56.2	3.9	2000	7	ADA71938	Ada71938 Rice gene
	37	51.2	3.5	1134	3	AAC45521	Aac45521 Arabidops
	38	50.8	3.5	1583	3	AAC45216	Aac45216 Arabidops
	39	50.8	3.5	1585	3	AAC33845	Aac33845 Arabidops
	40	50.8	3.5	1612	6	ABN98235	Abn98235 Arabidops
	41	50.4	3.5	6070	6	ABL32240	Ab132240 Human imm
	42	50.4	3.5	6070	6	ABL92198	Ab192198 Chemicall
	43	50.4	3.5	6070	6	ABL49309	Ab149309 Human pol
	44	50.2	3.5	71	6	ABK52088	Abk52088 Synthetic
C	45	49.6	3.4	1940	7	ABX77226	Abx77226 DNA sequ

ALIGNMENTS

RESULT 1
AAA61367
ID AAA61367 standard; DNA; 1444 BP.
XX
AC AAA61367;
XX
DT 06-NOV-2000 (first entry)
XX
DE Arabidopsis thaliana actin promoter region.
XX
KW Actin 2; ACT2; promoter; oxalate oxidase; OXOX; insecticidal; fungicidal;
KW antiviral; stability; ds.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT primer_bind complement(1..21)
FT primer_bind /*tag= a
FT primer_bind 1360..1379 /*tag= b
FT misc_signal 1382..1384 /*tag= c
FT /*note= "Translation start site for actin 2"

XX W0200037661-A1.
XX 29-JUN-2000.
XX 16-DEC-1999; 99WO-GB004317.
XX 21-DEC-1998; 98GB-00028201.
XX (ADVA-) ADVANTA TECHNOLOGY LTD.
XX Van Dun CMP, Schepers FMA, Pertijs JH;
XX WPI; 2000-442681/38.
XX Producing recombinant Compositae with increased transformation stability
XX comprises linking the DNA construct to the ACT2 gene promoter.
XX Claim 2; Fig 3; 22pp; English.
XX The present sequence is the promoter region and part of the coding
XX sequence of the Arabidopsis gene, actin 2 (ACT2). The promoter may be
XX used in a heterologous DNA construct to drive expression of RNA. This is

CC useful for the production of recombinant plants containing genes with
 CC insecticidal, fungicidal or antiviral activity. The advantage of using
 CC the ACT2 gene promoter is that it increases the stability of the
 CC integrated DNA. In the present invention the ACT2 promoter was used to
 CC drive expression of the wheat oxalate oxidase gene
 XX
 SQ Sequence 1444 BP; 451 A; 241 C; 272 G; 478 T; 0 U; 2 Other;

Query Match 99.9%; Score 1442; DB 3; Length 1444;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTATGATCTCAATACATTCATACATATCTCATAGATCTAGGTATCATATATGTAAG 60
 DB 1 ATTATGATCTCAATACATTCATACATATCTCATAGATCTAGGTATCATATATGTAAG 60

QY 61 AAGTTTTGACGAATATGNNACGACAAATGGCTACATCTCGATGTAATGGTATCTCAAC 120
 DB 61 AAGTTTTGACGAATATGNNACGACAAATGGCTACATCTCGATGTAATGGTATCTCAAC 120

QY 121 TCAACATTTACTTATACCAACATTTAGTTAGCAAAATTTAAACAACATTTATTTATGTAAT 180
 DB 121 TCAACATTTACTTATACCAACATTTAGTTAGCAAAATTTAAACAACATTTATTTATGTAAT 180

QY 181 GCAAGAGTCAGCATATGTAATTTGATTCAGATCGTTTGTGACGATTCGGATGTAGTAG 240
 DB 181 GCAAGAGTCAGCATATGTAATTTGATTCAGATCGTTTGTGACGATTCGGATGTAGTAG 240

QY 241 TAGCAATTTATTTAGTACATCTACTAATCTGTAATAGTATGATGATGAAACATTTGTATCTT 300
 DB 241 TAGCAATTTATTTAGTACATCTACTAATCTGTAATAGTATGATGATGAAACATTTGTATCTT 300

QY 301 ATTGTATAAATATTCATTAACACATCATCGAAGACATTTCTTTCAGGGTCTGAAATTAAT 360
 DB 301 ATTGTATAAATATTCATTAACACATCATCGAAGACATTTCTTTCAGGGTCTGAAATTAAT 360

QY 361 TATGATACAAATTTCTAATAGAAAACGAATTTAAATTACGTTGAATTTGATGAAATCTAATTG 420
 DB 361 TATGATACAAATTTCTAATAGAAAACGAATTTAAATTACGTTGAATTTGATGAAATCTAATTG 420

QY 421 AACAGCCCAACACGACGAGCTACGTTGCTGGATGACTTCGGTTTAGTTTACAC 480
 DB 421 AACAGCCCAACACGACGAGCTACGTTGCTGGATGACTTCGGTTTAGTTTACAC 480

QY 481 TAAAAAACGAGCTGTCTATTAACACGAGCTACGAGCTACAGTCAATGAGCAATC 540
 DB 481 TAAAAAACGAGCTGTCTATTAACACGAGCTACGAGCTACAGTCAATGAGCAATC 540

QY 541 AAGCAAAAAGAACTAATCCAGGGGTGAGATGATTAATTTAGTTTAAAAATTTAGTTAACAC 600
 DB 541 AAGCAAAAAGAACTAATCCAGGGGTGAGATGATTAATTTAGTTTAAAAATTTAGTTAACAC 600

QY 601 GAGGAAAAGCTGTCTGACAGCAGCTACGTTATCTTTACCTGTGGTGGAAATGATTCG 660
 DB 601 GAGGAAAAGCTGTCTGACAGCAGCTACGTTATCTTTACCTGTGGTGGAAATGATTCG 660

QY 661 TGTCTGTCGATTTTAAATTTATTTTGTAAAGGCCGAAAATAAAGTTGTAAGAGATAAAC 720
 DB 661 TGTCTGTCGATTTTAAATTTATTTTGTAAAGGCCGAAAATAAAGTTGTAAGAGATAAAC 720

QY 721 CGCCTATAAATTCATATATTTCTCCCGCTTTGAAATGTTCTCGTTTGTCTCTCTC 780
 DB 721 CGCCTATAAATTCATATATTTCTCCCGCTTTGAAATGTTCTCGTTTGTCTCTCTC 780

QY 781 TTTTCATCAGCCGTTTGAATCTCCGCGACTTGACAGAGAAACAGAGAAAGACTAA 840
 DB 781 TTTTCATCAGCCGTTTGAATCTCCGCGACTTGACAGAGAAACAGAGAAAGACTAA 840

QY 841 GAGAGAAAGTAAGATAATCCAGGAGATTCATTTCTCCGTTTGTGAATCTTCTCAATCTC 900
 DB 841 GAGAGAAAGTAAGATAATCCAGGAGATTCATTTCTCCGTTTGTGAATCTTCTCAATCTC 900

QY 901 ATCTTCTTCTCGCTCTTCTTTCACAGGTAATAGGAATCTTCTGGATCTACTTTATTT 960

DB 901 ATCTTCTTCTCGCTCTTCTTTCACAGGTAATAGGAATCTTCTGGATCTACTTTATTT 960

QY 961 GCTGGATCTCGATCTTGTGTTTCTCAATTTCTTGAGATCTCGGAATTCGTTAAATGGAT 1020

DB 961 GCTGGATCTCGATCTTGTGTTTCTCAATTTCTTGAGATCTCGGAATTCGTTAAATGGAT 1020

QY 1021 CTGTCGACCTCCACATAATCTTTTGGTTTACTAGATCGATTAAGTTGACCGATCAGT 1080

DB 1021 CTGTCGACCTCCACATAATCTTTTGGTTTACTAGATCGATTAAGTTGACCGATCAGT 1080

QY 1081 TAGCTCGATTTATAGCTACCAAAATTTGGCTTGACCTTGATGGAGAGATCCATGTTCAATG 1140

DB 1081 TAGCTCGATTTATAGCTACCAAAATTTGGCTTGACCTTGATGGAGAGATCCATGTTCAATG 1140

QY 1141 TACCTGGAAAATGATTGTATATGTAATTTGAAATCTGAACTGTTGAAATTTAGATTAAT 1200

DB 1141 TACCTGGAAAATGATTGTATATGTAATTTGAAATCTGAACTGTTGAAATTTAGATTAAT 1200

QY 1201 CTGAAACACTGTCAATGTTTAGATTAATCTGAAACACTGTTTAACTTAGATGAAGTTTGTG 1260

DB 1201 CTGAAACACTGTCAATGTTTAGATTAATCTGAAACACTGTTTAACTTAGATGAAGTTTGTG 1260

QY 1261 ATAGATTTCTCGAAACCTTAGGATTTGTAGTGTGCTAGCTTGAACAGAAAGCTATTTCTG 1320

DB 1261 ATAGATTTCTCGAAACCTTAGGATTTGTAGTGTGCTAGCTTGAACAGAAAGCTATTTCTG 1320

QY 1321 ATTCAATCAGGGTTTTATTTGACTGTAATTTGAACTCTTTTGTGTTGCACTCATAAA 1380

DB 1321 ATTCAATCAGGGTTTTATTTGACTGTAATTTGAACTCTTTTGTGTTGCACTCATAAA 1380

QY 1381 AATGGCTGAGGCTGACGATATTCACCAATCTGTGTGACATGCTTGAATGCTGGAATGCTAGG 1440

DB 1381 AATGGCTGAGGCTGACGATATTCACCAATCTGTGTGACATGCTTGAATGCTGGAATGCTAGG 1440

QY 1441 ATCC 1444

DB 1441 ATCC 1444

RESULT 2

ABK89341

ID ABK89341 standard; DNA; 6385 BP.

XX ABK89341;

XX 21-OCT-2002 (first entry)

XX Plasmid pACT2B-GUS DNA.

XX Arsenate reductase; ArsC; cyclic; circular; ds; antimonate; zinc;
 XX cadmium; phytochelatin biosynthetic enzyme; arsinite; cobalt;
 XX copper; mercury; antimony; soil; sediment; mine tailing; water; air;
 XX industrial waste; phytoremediation.

XX Synthetic.

XX WO200248335-A2.

XX 20-JUN-2002.

XX 13-DEC-2001; 2001WO-US048105.

XX 13-DEC-2000; 2000US-0255001P.

XX 22-JUN-2001; 2001US-0300525P.

XX (UYGE-) UNIV GEORGIA RES FOUND INC.

XX Meagher RB, Li Y;

XX WPI; 2002-583507/62.

XX Recombinant DNA molecules for producing transgenic plants tolerant to

KW industrial waste; phytoremediation.
 OS Synthetic.
 XX WO200248335-A2.
 PN 20-JUN-2002.
 PD 13-DEC-2001; 2001WO-US048105.
 XX 13-DEC-2000; 2000US-0255001P.
 PR 22-JUN-2001; 2001US-0300525P.
 XX (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA Meagher RB, Li Y;
 XX WPI; 2002-583507/62.
 DR Recombinant DNA molecules for producing transgenic plants tolerant to
 XX heavy metal ions, e.g. cadmium, arsenate, useful for phytoremediation of
 PT contaminated soil or water, encodes arsenate reductase coding sequence.
 PT Disclosure; Fig 12B; 131pp; English.
 XX The invention relates to a nucleic acid molecule comprising a portion
 CC encoding an arsenate reductase coding sequence and a plant-expressible
 CC transcription regulatory sequence, the coding sequence being operably
 CC linked to the transcription regulatory sequence. The nucleic acid is
 CC useful for producing a plant which is resistant to at least one metal ion
 CC such as a divalent cadmium ion or antimonate, by introducing the nucleic
 CC acid molecule into a plant cell or into plant tissue, selecting for the
 CC presence of the nucleic acid molecule to produce a transgenic plant cell
 CC or plant tissue and regenerating a plant from the transgenic plant cell
 CC or plant tissue. The method further comprises introducing at least one
 CC plant expressible phytochelatins biosynthetic enzyme coding sequence into
 CC the cell to produce an arsenate metal ion resistant plant. The arsenate
 CC reductase coding sequence is expressed under the control of a plant
 CC promoter which directs expression in the above ground plant part. The
 CC plant is also resistant to cadmium, cobalt, copper, mercury, zinc,
 CC antimony, arsenate and arsenite ions. The transgenic plant is useful for
 CC bioremediation of arsenate and/or cadmium-contaminated environments,
 CC including soil, sediments, mine tailings, water, industrial waste,
 CC groundwater and air. The transgenics are also useful for revegetation of
 CC soils contaminated with metal ions and for removing and sequestering
 CC these ions from water, wastewater and aqueous environments. The plants
 CC are also useful for phytoremediation of contaminated soil, sediment,
 CC water and mine tailings. This sequence represents plasmid pACT2B DNA,
 CC used in the scope of the invention
 XX
 XX Sequence 4526 BP; 1203 A; 997 C; 1002 G; 1321 T; 0 U; 3 Other;
 Query Match 92.98; Score 1341.4; DB 6; Length 4526;
 Best Local Similarity 98.98; Pred. No. 4.2e-314;
 Matches 1374; Conservative 0; Mismatches 11; Indels 4; Gaps 2;
 QY 1 ATTATGATCTCAATATGATATATCTATCTATGATCTAGATCTAGGTTATCATTTATGTAAG 60
 Db 257 ATTATGATCTCAATATGATATATCTATCTATGATCTAGATCTAGGTTATCATTTATGTAAG 316
 QY 61 AAAGTTTGGAGATATGNNACGACAAATGGCTACACTCGATGTAATTTGGTATCTCAAC 120
 Db 317 AAAGTTTGGAGATATGNNACGACAAATGGCTAGACTCGATGTAATTTGGTATCTCAAC 376
 QY 121 TCAACATATATCTTATACCAACATTTAGTACCAATTTTAAACACTATTTTATGAT 180
 Db 377 TCAACATATATCTTATACCAACATTTAGTACCAATTTTAAACACTATTTTATGAT 436
 QY 181 GCAAGAGTCAGCATATGATATGATTTGATTCAGATTCGTTTTCAGAGTTTCGGATGTAGTAG 240
 Db 437 GCAAGAGTCAGCATATGATATGATTTGATTCAGATTCGTTTTCAGAGTTTCGGATGTAGTAG 496
 QY 241 TAGCCATTTATTTATGATACATATCTAATCGTGAATAGTATGATGAAACATTTGATCTT 300

Db 497 TAGCCATTTATTTATGATACATATCTAATCGTGAATAGTATGATGAAACATTTGATCTT 556
 QY 301 ATTGTATAAATATCAATAAACAATCATCATGAAGACACTTTCTTCAGGGTCTGAATTAAT 360
 Db 557 ATTGTATAAATATCAATAAACAATCATCATGAAGACACTTTCTTCAGGGTCTGAATTAAT 616
 QY 361 TAGGATACAAATTTCTAATAGAAAGAAATTAATTTACGTTGAATTTATGAATCTTAATTTG 420
 Db 617 TAGGATACAAATTTCTAATAGAAAGAAATTAATTTACGTTGAATTTATGAATCTTAATTTG 676
 QY 421 AACAAAGCCAAACCCAGCAGCAGCTTAACGTTGCTGGATTCGCTGTTTAAGTTAAACCAAC 480
 Db 677 AACAAAGCCAAACCCAGCAGCAGCTTAACGTTGCTGGATTCGCTGTTTAAGTTAAACCAAC 736
 QY 481 TAAAAAAACCGAGCTGTCATGTAAACACCGGATCGAGCAGCTCACAGTCATGAAGCCATC 540
 Db 737 TAAAAAAACCGAGCTGTCATGTAAACACCGGATCGAGCAGCTCACAGTCATGAAGCCATC 796
 QY 541 AAAGCAAAAGAACTAATCCAAAGGGTGAATTAATTAAGTTTAAATTAAGTTAAGTTAAGCAAC 600
 Db 797 AAAGCAAAAGAACTAATCCAAAGGGTGAATTAATTAAGTTTAAATTAAGTTAAGTTAAGCAAC 856
 QY 601 GAGGAAAAA-GGTGTCTGTACAGCCAGCTCACGTTATCTTTTACCTGTGCTCGAAATGATTC 659
 Db 857 GAGGAAAAAAGGCTGTCTGACAGCCAGCTCACGTTATCTTTTACCTGTGCTCGAAATGATTC 916
 QY 660 GTGTCTGTGATTTTAAATTAATTTTGAAGGGCGGAAATTAAGTTTGAAGAGTAACAC 719
 Db 917 GTGTCTGTGATTTTAAATTAATTTTGAAGGGCGGAAATTAAGTTTGAAGAGTAACAC 976
 QY 720 CCGCTATATAAATTCATATATTTTCCCTCCCGCTTTGAATTTGCTCGTTCTCTCTCTCA 779
 Db 977 CCGCTATATAAATTCATATATTTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 1036
 QY 780 CTTTCATCAGCGGTTTGAATCTCCGGGCACTTCACAGAGAGAAACAAGAGAGAACTA 839
 Db 1037 CTTTCATCAGCGGTTTGAATCTCCGGGCACTTCACAGAGAGAAACAAGAGAGAACTA 1096
 QY 840 AGAGAGAAAGTAAGAGATATCCAGAGATTCATCTCCGTTTGAATCTTCCTCTCAATCT 899
 Db 1097 AGAGAGAAAGTAAGAGATATCCAGAGATTCATCTCCGTTTGAATCTTCCTCTCAATCT 1156
 QY 900 CATCTCTCTCTCCGCTCTTTCTTCCAGAGTAATAGAACTTCTCGATCTACTTTAT 959
 Db 1157 CA---TCCTCTCTCGCTCTTTCTTCCAGAGTAATAGAACTTCTCGATCTACTTTAT 1213
 QY 960 TGCTGATCTGATCTGTTTCTCAATTTCTTGAAGATCTCGAAATTCGTTTAAATTTGGA 1019
 Db 1214 TGCTGATCTGATCTGTTTCTCAATTTCTTGAAGATCTCGAAATTCGTTTAAATTTGGA 1273
 QY 1020 TCTGTGAACCTCCACTAAATCTTTTGGTTTCTTACGATCTAGTTCGATCGATCGATCAG 1079
 Db 1274 TCTGTGAACCTCCACTAAATCTTTTGGTTTCTTACGATCTAGTTCGATCGATCGATCAG 1333
 QY 1080 TTAGCTCGATTTATAGCTACACAAATTTGGCTTGAACCTTGAATCGAGAGATCCATGTTTCA 1139
 Db 1334 TTAGCTCGATTTATAGCTACACAAATTTGGCTTGAACCTTGAATCGAGAGATCCATGTTTCA 1393
 QY 1140 TTACCTGGGAAATGATTTGATATGTAATTTGAATTTGAAATCTGAACTGTTGAAGTTAGATGAA 1199
 Db 1394 TTACCTGGGAAATGATTTGATATGTAATTTGAATTTGAAATCTGAACTGTTGAAGTTAGATGAA 1453
 QY 1200 TCTGACACTGCTCAATCTAGATTTGAATCTGAACTGTTTAAAGTTAGATGAAATTTTGG 1259
 Db 1454 TCTGAAACCTGCTCAATCTAGATTTGAATCTGAACTGTTTAAAGTTAGATGAAATTTTGG 1513
 QY 1260 TATAGATTTCTCGAAACCTTTAGGATTTTGTAGTCTGCTAGCTTGAACAGAAAGCTATTTCT 1319
 Db 1514 TATAGATTTCTCGAAACCTTTAGGATTTTGTAGTCTGCTAGCTTGAACAGAAAGCTATTTCT 1573
 QY 1320 GATTCAATCAGGGTTTATTTGATCTGATTTGAATCTCTTTTGTGTTGTTGAGCTCATAAA 1379

QY 957 ATTTGCTGAGCTGATCTGTTTCTCAATTTCCCTTGAGATCGAATCGTTTAAATTT 1016
 Db 1050 ATTGCTGAGCTGATCTGTTTCTCAATTTCCCTTGAGATCGAATCGTTTAAATTT 1109
 QY 1017 GGATCTGTGAACCTCCACTAAATCTTTTGGTTTTACTAGAAATCGATCTAAAGTTGACCGAT 1076
 Db 1110 GGATCTGTGAACCTCCACTAAATCTTTTGGTTTTACTAGAAATCGATCTAAAGTTGACCGAT 1169
 QY 1077 CAGTTAGCTGATTTATAGCTACAGAAATTTGGCTTGACCTTGATGGAGAGATCATGTTTC 1136
 Db 1170 CAGTTAGCTGATTTATAGCTACAGAAATTTGGCTTGACCTTGATGGAGAGATCATGTTTC 1229
 QY 1137 ATGTTACCTGGGAATGATTTGTATATGTGAATTTGAATCTGAATCTGTTGAAGTTAGATT 1196
 Db 1230 ATGTTACCTGGGAATGATTTGTATATGTGAATTTGAATCTGTTGAAGTTAGATT 1299
 QY 1197 GAATCTGAACACTGTCATCTGATTTAGATTTGAATCTGAACTGTTTAAAGTTAGATCAAGTTT 1256
 Db 1290 GAATCTGAACACTGTCATCTGATTTAGATTTGAATCTGAACTGTTTAAAGTTAGATCAAGTTT 1349
 QY 1257 GTGTATAGATTTCTGAACTTGAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1316
 Db 1350 GTGTATAGATTTCTGAACTTGAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1409
 QY 1317 TCTGATTCATCAGGGTTTATTTGACTGTATTTGAATCTGTTTGTGTTGTTGCTGAGCTCAT 1376
 Db 1410 TCTGATTCATCAGGGTTTATTTGACTGTATTTGAATCTGTTTGTGTTGTTGCTGAGCTCAT 1469
 QY 1377 AAAAA 1381
 Db 1470 AAAAA 1474

RESULT 5
 ID ABK89343 standard; DNA; 3450 BP.
 XX
 AC ABK89343;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Plasmid pECSACT2 DNA.
 XX
 KW Arsenate reductase; ArsC; cyclic; circular; ds; antimonate; zinc;
 KW cadmium; phytochelatin biosynthetic enzyme; arsenite; cobalt;
 KW copper; mercury; antimony; soil; sediment; mine tailing; water; air;
 KW industrial waste; phytoremediation.
 XX
 OS Synthetic.
 XX
 PN WO200248335-A2.
 XX
 PD 20-JUN-2002.
 XX
 PF 13-DEC-2001; 2001WO-US048105.
 XX
 PR 13-DEC-2000; 2000US-0255001P.
 PR 22-JUN-2001; 2001US-0300525P.
 XX
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 XX
 PI Meagher RB, Li Y;
 XX
 WPI; 2002-583507/62.
 XX
 PT Recombinant DNA molecules for producing transgenic plants tolerant to
 PT heavy metal ions, e.g. cadmium, arsenate, useful for phytoremediation of
 PT contaminated soil or water, encodes arsenate reductase coding sequence.
 XX
 PS Disclosure; Page 75-77; 131pp; English.
 XX
 CC The invention relates to a nucleic acid molecule comprising a portion

CC encoding an arsenate reductase coding sequence and a plant-expressible
 CC transcription regulatory sequence, the coding sequence being operably
 CC linked to the transcription regulatory sequence. The nucleic acid is
 CC useful for producing a plant which is resistant to at least one metal ion
 CC such as a divalent cadmium ion or antimonate, by introducing the nucleic
 CC acid molecule into a plant cell or into plant tissue, selecting for the
 CC presence of the nucleic acid molecule to produce a transgenic plant cell
 CC or plant tissue and regenerating a plant from the transgenic plant cell
 CC or plant tissue. The method further comprises introducing at least one
 CC plant expressible phytochelatin biosynthetic enzyme coding sequence into
 CC the cell to produce an arsenate metal ion resistant plant. The arsenate
 CC reductase coding sequence is expressed under the control of a plant
 CC promoter which directs expression in the above ground plant part. The
 CC plant is also resistant to cadmium, cobalt, copper, mercury, zinc,
 CC antimony, arsenate and arsenite ions. The transgenic plant is useful for
 CC bioremediation of arsenate and/or cadmium-contaminated environments,
 CC including soil, sediments, mine tailings, water, industrial waste,
 CC groundwater and air. The transgenics are also useful for revegetation of
 CC soils contaminated with metal ions and for removing and sequestering
 CC these ions from water, wastewater and aqueous environments. The plants
 CC are also useful for phytoremediation of contaminated soil, sediment,
 CC water and mine tailings. This sequence represents plasmid pECSACT2 DNA,
 CC used in the scope of the invention
 XX
 SQ Sequence 3450 BP; 946 A; 694 C; 764 G; 1046 T; 0 U; 0 Other;
 Query Match 89.9%; Score 1298.4; DB 6; Length 3450;
 Best Local Similarity 98.1%; Pred. NO. 1.1e-303; Indels 8; Gaps 6;
 Matches 1376; Conservative 0; Mismatches 18;
 QY 1 ATATGATCTCAATACATTTGATACATATCTCATCTAGATCTAGGTTATCATTTATGTAAG 60
 Db 9 ATGCTGATCTCAATACATTTGATACATATCTCATCTAGATCTAGGTTATCATTTATGTAAG 68
 QY 61 AAGTTTTGACGAATATGNNACGAAATATGGCTACACTCGATGTAATGGTATCTCAAC 120
 Db 69 AAGTTTTGACGAATATGGCAGCAAAATATGGCTAGACTCGATGTAATGGTATCTCAAC 128
 QY 121 TCAACATTTACTTATACCAACATTTAGTTAG-CAAAATTTAAACAACATA-TTTTTATGT 178
 Db 129 TCAACATTTACTTATACCAACATTTAGTTAGACAAAATTTAAACAACATA-TTTTTATGT 188
 QY 179 ATGCAAGAGTACGATATGTAATTAATGATTCAGAAATCGTTTTGACGAGTTCGGATGTAGT 238
 Db 189 ATGCAAGAGTACGATATGTAATTAATGATTCAGAAATCGTTTTGACGAGTTCGGATGTAGT 248
 QY 239 AGTAGGCAATTTTAAATGATACATCTAATTCGTAATAGTG-ATAATGATGAACAATTTGAT 297
 Db 249 AGTAGGCAATTTTAAATGATACATCTAATTCGTAATAGTGAAATGATGTAACAATTTGAT 308
 QY 298 CTTATTTGATAAATATCCATAAACAATCATGTAAGACACTTTTCTTCAGGGTCTGAAT 357
 Db 309 CTTATTTGATAAATATCCATAAACAATCATGTAAGACACTTTTCTTCAGGGTCTGAAT 368
 QY 358 AATTATGATACAAATTTCTAATAGAAAACGAAATTAATTAACGTTGAATTTGATGAATCTAA 417
 Db 369 AATTATGATACAAATTTCTAATAGAAAACGAAATTAATTAACGTTGAATTTGATGAATCTAA 428
 QY 418 TTGACAGAGCAACCAACGAGAGGACTAATCGTTGCGGATTTGACTCGGTTTAGTTAAC 477
 Db 429 TTGACAGAGCAACCAACGAGAGGACTAATCGTTGCGGATTTGACTCGGTTTAGTTAAC 488
 QY 478 CACTAAAAAAGCGAGCTGTCTATGTAACACCGGATCGAGCAGGTACAGTCATGAAGCC 537
 Db 489 CACTAAAAAAGCGAGCTGTCTATGTAACACCGGATCGAGCAGGTACAGTCATGAAGCC 548
 QY 538 ATCAAGCAAAAAGAACTAAATCCAAAGGGGTGAGATGATTAAATAGTTTAAAAATGATTAA 597
 Db 549 ATCAAGCAAAAAGAACTAAATCCAAAGGGGTGAGATGATTAAATAGTTTAAAAATGATTAA 608
 QY 598 CACGAGGAAAAA-GCTGTCTGACAGCAGGCTCAGTTATCTTTTACCTGTGTCGAATGA 656
 Db 609 CACGAGGAAAAAGGCTGTCTGACAGCAGGCTCAGTTATCTTTTACCTGTGTCGAATGA 668

QY 657 TTCGTGCTGCTGATTTTAAATTTTGTGAAAGCGCGAAATAAAGTGTGAAGAGATA 716
 Db 669 TTCGTGCTGCTGATTTTAAATTTTGTGAAAGCGCGAAATAAAGTGTGAAGAGATA 728
 QY 717 AACCCGCTATATAAATTCATATATTTTCTCCCGCTTTTGAATTTGCTGCTGCTGCTCC 776
 Db 729 AACCCGCTATATAAATTCATATATTTTCTCCCGCTTTGAAATTTGCTGCTGCTGCTCC 788
 QY 777 TCACCTTTCATCAGCGCTTTGAATCTCCGCGACTTCGACAGAGAACAGAGAGAGAGA 836
 Db 789 TCACCTTTCATCAGCGCTTTGAATCTCCGCGACTTCGACAGAGAACAGAGAGAGAGA 848
 QY 837 CTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATCTCCGCTTTTGAATTTTCTCCCAA 896
 Db 849 CTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATCTCCGCTTTTGAATTTTCTCCCAA 908
 QY 897 TCTCATCTTCTTCTCCGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 956
 Db 909 TCTCA--TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 965
 QY 957 ATTGCTGCTGATCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1016
 Db 966 ATTGCTGCTGATCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1025
 QY 1017 GGATCTGGAACCTCCACTAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1076
 Db 1026 GGATCTGGAACCTCCACTAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1085
 QY 1077 CAGTAGCTGATATAGCTACAGAAATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1136
 Db 1086 CAGTAGCTGATATAGCTACAGAAATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1145
 QY 1137 ATGTTACTGCGGAATGATTTGTATATGTGAATCTGAATCTGAATCTGAATCTGAATCTGA 1196
 Db 1146 ATGTTACTGCGGAATGATTTGTATATGTGAATCTGAATCTGAATCTGAATCTGAATCTGA 1205
 QY 1197 GAATCTGAACACTGTCAATGTAGATTAATCTGAACACTGTCAATGTAGATTAATCTGAACACT 1255
 Db 1206 GAATCTGAACACTGTCAATGTAGATTAATCTGAACACTGTCAATGTAGATTAATCTGAACACT 1265
 QY 1256 TGCTGATAGATTTCTGAAACCTTAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1315
 Db 1266 TGCTGATAGATTTCTGAAACCTTAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1325
 QY 1316 TTCTGATTCATCAGGGTTTATTGACTCTATTGAACTCTTTTGTGTTGTTGCTGCTGCTGCT 1375
 Db 1326 TTCTGATTCATCAGGGTTTATTGACTCTATTGAACTCTTTTGTGTTGTTGCTGCTGCTGCT 1385
 QY 1376 TAAAAAATGGCTGAGCGTGAAG 1397
 Db 1386 TAAACCATGGCAATCCCGAGC 1407

RESULT 6
 ABK9342
 ID ABK9342 standard; DNA; 3408 BP.
 XX
 AC ABK9342;
 XX
 XX
 DT 21-OCT-2002 (first entry)
 XX
 XX Plasmid pAtPCSACT2 DNA.
 XX
 XX Arsenate reductase; ArsC; cyclic; circular; ds; antimionate; zinc;
 KW cadmium; phytochelatin biosynthetic enzyme; arsenite; arsenite; cobalt;
 KW copper; mercury; antimony; soil; sediment; mine tailing; water; air;
 KW industrial waste; phytoremediation.
 XX
 OS Synthetic.
 OS
 XX
 XX WO200248335-A2.
 XX

PD 20-JUN-2002.
 XX
 XX 13-DEC-2001; 2001WO-US048105.
 XX
 PR 13-DEC-2000; 2000US-0255001P.
 PR 22-JUN-2001; 2001US-0300525P.
 XX
 PA (UVRB-) UNIV GEORGIA RES FOUND INC.
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 XX Meagher RB, Li Y;
 PI WPI; 2002-583507/62.
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 PT contaminated soil or water, encodes arsenate reductase coding sequence.
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 CC or plant tissue and regenerating a plant from the transgenic plant cell
 CC or plant tissue. The method further comprises introducing at least one
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 CC the cell to produce an arsenate metal ion resistant plant. The arsenate
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 CC promoter which directs expression in the above ground plant part. The
 CC plant is also resistant to cadmium, cobalt, copper, mercury, zinc,
 CC antimony, arsenate and arsenite ions. The transgenic plant is useful for
 CC bioremediation of arsenate and/or cadmium-contaminated environments,
 CC including soil, sediments, mine tailings, water, industrial waste,
 CC groundwater and air. The transgenics are also useful for revegetating
 CC soils contaminated with metal ions and for removing and sequestering
 CC these ions from water, wastewater and aqueous environments. The plants
 CC are also useful for phytoremediation of contaminated soil, sediment,
 CC water and mine tailings. This sequence represents plasmid pAtPCSACT2 DNA,
 CC used in the scope of the invention
 XX
 SQ Sequence 3408 BP; 980 A; 638 C; 693 G; 1097 T; 0 U; 0 Other;
 Query Match 89.8%; Score 1297.4; DB 6; Length 3408;
 Best Local Similarity 98.5%; Pred. No. 1.9e-303; Mismatches 13; Indels 8; Gaps 6;
 Matches 1372; Conservative 0;
 QY 1 ATTATGATCTCAAATACATTCATATATCTCATCTAGATCTAGGTTATCATTTATGTAAG 60
 Db 9 ATGCTGATCTCAAATACATTCATATATCTCATCTAGATCTAGGTTATCATTTATGTAAG 68
 QY 61 AAAGTTTGGAGATATGNNACGACAAATGGCTACACTCGATGTAATGGTATCTCAAC 120
 Db 69 AAAGTTTGGAGATATGNNACGACAAATGGCTACACTCGATGTAATGGTATCTCAAC 128
 QY 121 TCAACATTAATCTTATACCAACATTTAGTAGTAAATTTTAAACACTA-TTTTTATGT 178
 Db 129 TCAACATTAATCTTATACCAACATTTAGTAGTAAATTTTAAACACTA-TTTTTATGT 188
 QY 179 ATGCAAGATCGACATATGTAATTTGATTCAGAAATCGTTTTCAGGATTCGGATGTAGT 238
 Db 189 ATGCAAGATCGACATATGTAATTTGATTCAGAAATCGTTTTCAGGATTCGGATGTAGT 248
 QY 239 AGTAGCAATTTATTTAATGTAATCTAATTCGTGAATAGTG-ATATGATGAACATTTGAT 297
 Db 249 AGTAGCAATTTATTTAATGTAATCTAATTCGTGAATAGTG-ATATGATGAACATTTGAT 308
 QY 298 CTTATTTGTAATAATTCATTAACACATCATCAAGACACTTTTCTTTCAGGCTCTGAAT 357
 Db 309 CTTATTTGTAATAATTCATTAACACATCATCAAGACACTTTTCTTTCAGGCTCTGAAT 368

QY	61	AAAGTTTTGACGAAATATGNNACGACAAATATGCTACACTCGATGTAAATTTGGTATCTCAAC	120
DB	69	AAAGTTTTGACGAAATATGCGACGACAAATATGCTAGACTCGATGTAAATTTGGTATCTCAAC	128
QY	121	TCAACATTATACATTATACCAACAACTTAGTTAG-CAAAATTTTAAACAACATC-TTTTTTGT	178
DB	129	TCAACATTATACATTATACCAACAACTTAGTTAGTGTACAAAATTTTAAACAACATTTTATGT	188
QY	179	ATGCAAGAGTCAGCATATGTATAATTCGANTCAGAAATCGTTTTGACGAGTCGGATGTAGT	238
DB	189	ATGCAAGAGTCAGCATATGTATAATTCGANTCAGAAATCGTTTTGACGAGTCGGATGTAGT	248
QY	239	AGTAGCGATTTATTAATGTACATATCTAATCTGTGTAATAGTG-ATATGATGAAAACATTTGTAT	297
DB	249	AGTAGCGATTTATTAATGTACATATCTAATCTGTGTAATAGTGAATATGATGAAAACATTTGTAT	308
QY	298	CTTATTGTATAAATATCCATAAACAATCATCATCAAAAGACATCTTCTTCAGGGTCTCGAATT	357
DB	309	CTTATTGTATAAATATCCATAAACAATCATCATCAAAAGACATCTTCTTCAGGGTCTCGAATT	368
QY	358	AATTAATGATACAATCTTAATAGAAAACGAATTTAAATTCGTTGAAATCTGATGAAATCTTAA	417
DB	369	AATTAATGATACAATCTTAATAGAAAACGAATTTAAATTCGTTGAAATCTGATGAAATCTTAA	428
QY	418	TTGACACAGCCACACGACGACGAGACTACGTTGCTGTGATTCGACTCGGTTTAAGTTAAAC	477
DB	429	TTGACACAGCCACACGACGACGAGACTACGTTGCTGTGATTCGACTCGGTTTAAGTTAAAC	488
QY	478	CACATAAAAAACGGAGCTGTCACTATACACGGGATCGACAGGTCAAGTCATGAAGCC	537
DB	489	CACATAAAAAACGGAGCTGTCACTATACACGGGATCGACAGGTCAAGTCATGAAGCC	548
QY	538	ATCAAAGCAAAGAACCTAATCAAGGGGTGAGATGATTAATAGTTTAAAAAATTAGTTAA	597
DB	549	ATCAAAGCAAAGAACCTAATCAAGGGGTGAGATGATTAATAGTTTAAAAAATTAGTTAA	608
QY	598	CACGAGGAAAA-GCTGTCTGCACAGCCAGGTCAAGTTATCTTTTACCTGTGTGTCGTAATGA	656
DB	609	CACGAGGAAAAAGCGTGTCTGCACAGCCAGGTCAAGTTATCTTTTACCTGTGTGTCGTAATGA	668
QY	657	TTGCTGTCTGTGCAATTTAAATATTTTTTTTAAAGGCCGAAATAAAGTGTAAAGAGATA	716
DB	669	TTGCTGTCTGTGCAATTTAAATATTTTTTTTAAAGGCCGAAATAAAGTGTAAAGAGATA	728
QY	717	AACCGGCTATATAAATTCATATATTTCTCCCGGCTTTGAAATGTCTCGTTGTCTCTCC	776
DB	729	AACCGGCTATATAAATTCATATATTTCTCTCCCGCTTTGAAATGTCTCGTTGTCTCTCC	788
QY	777	TCACATTCATCAGCGGTTTTGAATCTCCGCGACTTCGACGAGAGACACAGGAGAGA	836
DB	789	TCACATTCATCAGCGGTTTTGAATCTCCGCGACTTCGACGAGAGACACAGGAGAGA	848
QY	837	CTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTCTCCGTTTTTGAATCTTCTCTCAA	896
DB	849	CTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTCTCCGTTTTTGAATCTTCTCTCAA	908
QY	897	TCTCATCTTCTTCTTCGCGCTCTTCTTCTTCCAAAGGTAAATAGAACCTTTCGATCTACTT	956
DB	909	TCTCTCA---TCTTCTTCGCGCTCTTCTTCTTCCAAAGGTAAATAGAACCTTTCGATCTACTT	965
QY	957	ATTTCGTCGATCTCGATCTGTTTTCTCAATTTCTTTCGATCTCGAATTCGTTTAAATTT	1016
DB	966	ATTTCGTCGATCTCGATCTGTTTTCTCAATTTCTTTCGATCTCGAATTCGTTTAAATTT	1025
QY	1017	GGATCTGTGAACCTCCACTAAATCTTTTGGTTTTTACTAGAAATCGATCTAAGTTGACCGAT	1076
DB	1026	GGATCTGTGAACCTCCACTAAATCTTTTGGTTTTTACTAGAAATCGATCTAAGTTGACCGAT	1085
QY	1077	CAGTAGCTCGAATATAGCTACAGAAATTTGCTGTGACCTTGATCGAGAGATCCATGTTTC	1136
DB	1086	CAGTAGCTCGAATATAGCTACAGAAATTTGCTGTGACCTTGATCGAGAGATCCATGTTTC	1145

RESULT 8

RESULT 8
AAD09791

AAD09791
ID AAD09791 standard: DNA: 1219 BP.

ID
XX
AAD09791

XX
AC
AAD09791.

AC AAD09791;
YYXX
DT 10-SEP-20DT 10-SEP-20
VV

DE Arabidopsis thaliana Act2 promoter including intron of Act2 gene.

XX	2000
XX	2000

KW DNA const 2.07e-01

KW Act; elon
KW Ambat

KW glyphosat

KW PCR prime

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OS Arabidops
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X

FH **Key**

FT promoter

III

LE

FT misc_sign

LE

LET

FT intron

FT 1000

XXIX

PN WO2001444

XX
NY
NY 10070

PD 21-JUN-20

FD 21-JUN-20
XX

12-DEC-20

XX
12-DEC-20
PF

PR 16-DEC-19

XX
16-DEC-19

XX DA (MONIC) M

CC operably linked to SG. The present invention further relates to plant
CC expression constructs that comprise Arabidopsis actin (Act) promoter
CC sequences Actia, Actb, Act3, Act7, Act11, Act12, elongation
CC factor 1 alpha (E1alpha) promoter sequence, fragments and cis elements
CC derived from these promoters operably linked to heterologous structural
CC gene sequences that function in crop plant cells. The DNA constructs are
CC useful for controlling weeds, by providing a crop plant transformed with
CC DNA construct comprising promoter DNA sequence that is functional in a
CC plant cell, a glyphosate tolerance gene (which is an EPSP synthase gene
CC or a glyphosate oxidoreductase gene) or a herbicide tolerance gene. The
CC present sequence is Arabidopsis thaliana Act2 promoter including intron
CC of Act2 gene
XX

SQ Sequence 1219 BP; 370 A; 207 C; 233 G; 409 T; 0 U; 0 Other;

Query Match 81.4%; Score 1174.8; DB 4; Length 1219;
Best Local Similarity 98.7%; Pred. No. 5.9e-274;
Matches 1206; Conservative 0; Mismatches 12; Indels 4; Gaps 2;

QY 164 CAACATATTTTATGATGCAAGAGTCAGCATATGTATAATTGATTCAGAACTCGTTTGAC 223
DB 1 CAACATATTTTATGATGCAAGAGTCAGCATATGTATAATTGATTCAGAACTCGTTTGAC 60
QY 224 GAGTTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 283
DB 61 GAGTTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
QY 284 ATGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 343
DB 121 ATGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 344 TCAGGGTCGTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 403
DB 181 TCAGGGTCGTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 404 TGTATGAATCTTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 463
DB 241 TGTATGAATCTTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 464 CGGTTTAAGTTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 523
DB 301 CGGTTTAAGTTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 524 ACAGTCATGAAGCCATCAAGCAAAAGAACTAATCAAGGGGTGAGATGATTAATTAATGAT 583
DB 361 ACAGTCATGAAGCCATCAAGCAAAAGAACTAATCAAGGGGTGAGATGATTAATTAATGAT 420
QY 584 TAAAAATTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 642
DB 421 TAAAAATTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 643 TGTGTCGAAATGATTCGTGTCGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 702
DB 481 TGTGTCGAAATGATTCGTGTCGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 540
QY 703 AGTTGTAAGAGATAAACCAGCCATATAAATTAATTAATTAATTAATTAATTAATTAATTAAT 762
DB 541 AGTTGTAAGAGATAAACCAGCCATATAAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
QY 763 TCTCGTTGTCCTTCCTCACTTTCATCAGCCGTTTGAATCTCCGGGACCTTTCAGAGAGAG 822
DB 601 TCTCGTTGTCCTTCCTCACTTTCATCAGCCGTTTGAATCTCCGGGACCTTTCAGAGAGAG 660
QY 823 AACAGGAAG 882
DB 661 AACAGGAAG 720
QY 883 TGAATCTTCTCAATCTCATCTTCTTCTTCCGCTCTTCTTCTTCCAGAGTAATAGAGAACT 942
DB 721 TGAATCTTCTCAATCTCATCTTCTTCTTCCGCTCTTCTTCTTCCAGAGTAATAGAGAACT 777
QY 943 TCTGATCTACTTATTTTGTGGATCTCGATCTGTTTCTCAATTTCTTCTTCTTCTTCTTCTTCT 1002

DB 778 TCTGATCTACTTATTTTGTGGATCTCGATCTGTTTCTCAATTTCTTCTTCTTCTTCTTCTG 837
QY 1003 AATTCGTTTAAATTTGATCTCTGAACTCCACTAAATCTTTTGGTTTACTAGAACTGAT 1062
DB 838 AATTCGTTTAAATTTGATCTCTGAACTCCACTAAATCTTTTGGTTTACTAGAACTGAT 897
QY 1063 CTAAAGTTGACCGATCAGTTCAGTATAGCTTACCTACCAAGATTTGGCTTGACCTTGATGG 1122
DB 898 CTAAAGTTGACCGATCAGTTCAGTATAGCTTACCTACCAAGATTTGGCTTGACCTTGATGG 957
QY 1123 AGAGATCCATGTTCTATGTTACCTGGGAAATGATTTGTATATGTGAATTTGAATCTGAACT 1182
DB 958 AGAGATCCATGTTCTATGTTACCTGGGAAATGATTTGTATATGTGAATTTGAATCTGAACT 1017
QY 1183 GTTGAAGTTAGATGAATCTGAACACTGTCATGTAGATTTGAATCTGAACACTGTTTAA 1242
DB 1018 GTTGAAGTTAGATGAATCTGAACACTGTCATGTAGATTTGAATCTGAACACTGTTTAA 1077
QY 1243 GTTGAAGTTAGATGAATCTGAACACTGTCATGTAGATTTGAATCTGAACACTGTTTAA 1302
DB 1078 GTTGAAGTTAGATGAATCTGAACACTGTCATGTAGATTTGAATCTGAACACTGTTTAA 1137
QY 1303 AACAGAAAGCTATTTCTGATTCATCAATCAGGGTTTATTTGACGTGATTTGAATCTTTTGTG 1362
DB 1138 AACAGAAAGCTATTTCTGATTCATCAATCAGGGTTTATTTGACGTGATTTGAATCTTTTGTG 1197
QY 1363 TGTGTCGAGCTCATAAAATG 1384
DB 1198 TGTGTCGAGCAGACTCACCATG 1219
RESULT 9
AAD09812
ID AAD09812 standard; DNA; 1742 BP.
XX
AC AAD09812;
XX
DT 11-SEP-2003 (revised)
DT 10-SEP-2001 (first entry)
XX
DE Chimeric CamV-Act2 promoter including first intron of Act2 gene.
XX DNA construct; structural gene; SG; non-translated region; NTR; actin;
XX Act; elongation factor 1 alpha; E1alpha; weed control; EPSP synthase;
XX glyphosate tolerance; glyphosate oxidoreductase; herbicide tolerance;
XX PCR primer; Act2 promoter; Cauliflower mosaic virus; CamV; chimeric; ds.
XX Cauliflower mosaic virus.
OS Arabidopsis thaliana.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT promoter 1..523 a
FT /note= "CamV promoter"
FT misc_feature 534..1742
FT /tag= b
FT /note= "Arabidopsis thaliana Act2 promoter, intron and 5'
FT UTR region"
XX
PN W0200144457-A2.
XX
PD 21-JUN-2001.
XX
PF 12-DEC-2000; 2000WO-US033633.
XX
PR 16-DEC-1999; 99US-0171173P.
XX (MONS) MONSANTO CO.
XX
PI Fincher KL, Flasiński S, Wilkinson JQ;
XX MPI; 2001-408480/43.
XX

FT CDS 1243..2895
FT /*tag= d
FT /product= "Luciferase"
FT polyA_site 2929..3570
FT /*tag= e
FT /note= "RbcS E9 polyA region"
XX WO200281647-A2.
XX
XX 17-OCT-2002.
XX
XX 08-APR-2002; 2002WO-US011116.
XX
XX 06-APR-2001; 2001US-02B2094P.
XX (Scri) SRIpps RES INST.
XX
XX Kay SA, Kuhlmann T, Lerner RA;
XX WPI; 2003-058526/05.
XX
XX Novel genetically modified plant cell, useful as research tool, comprises
PT a heterologous nucleotide sequence encoding a bioluminescent polypeptide
PT expressed in an amount sufficient to produce visible light.
XX
XX Claim 21; Page 90-96; 96pp; English.
XX
XX The present sequence is that of luciferase expression vector ACT-OM-LUC
CC comprising an expression construct composed of an actin 2 regulatory
CC element comprising an enhancer and promoter, a tobacco mosaic virus omega
CC translational enhancer, a nucleotide sequence encoding luciferase, and an
CC RbcS E9 polyA region. Claimed vectors, including ACT-OM-LUC, can be used
CC to transform a plant cell such that the cell expresses luciferase in an
CC amount sufficient to produce at least 750,000 photons of visible light/sq
CC mm/second. Also claimed are visibly bioluminescent transgenic plants that
CC contain the genetically modified plant cell. the transgenic plant may be
CC a monocot or dicot, including an angiosperm, cereal, legume, oilseed
CC plant or hardwood tree, or an ornamental plant such as petunia or
CC carnation (all claimed). The transgenic plants are useful as research
CC tools and have ornamental value
XX
XX Sequence 12304 BP; 2928 A; 3115 C; 3142 G; 3119 T; 0 U; 0 Other;
XX
Query Match 77.2%; Score 1114.6; DB 7; Length 12304;
Best Local Similarity 98.0%; Pred. No. 4.3e-259;
Matches 1150; Conservative 0; Mismatches 19; Indels 4; Gaps 2;
QY 224 GAGTTCGGATGTAGTAGGCAATTTTAAATGATACATACTAATCGTAATAGTAGATG 283
DB 1 GATCCCGGATGTAGTAGGCAATTTTAAATGATACATACTAATCGTAATAGTAGATG 60
QY 284 ATGAACATGTATCTTATTGTATATAATCCATAACACATCATGAAGACACTTTCT 343
DB 51 ATGAACATGTATCTTATTGTATATAATCCATAACACATCATGAAGACACTTTCT 120
QY 344 TCAGGTCTGAATTAATATGATGATCAATTTCTAATAGAAAACGAATTAATGCTTGAAT 403
DB 121 TCAGGTCTGAATTAATATGATGATCAATTTCTAATAGAAAACGAATTAATGCTTGAAT 180
QY 404 TGATGAAATCTTAATGAAACGCAACCAACGACGAGCACTACGTTGCTGATGACT 463
DB 181 TGATGAAATCTTAATGAAACGCAACCAACGACGAGCACTACGTTGCTGATGACT 240
QY 464 CGGTTTAAGTTAAACCATTAATAAAGGAGCTGTGATGATCAACGCGGATCGAGCGGTC 523
DB 241 CGGTTTAAGTTAAACCATTAATAAAGGAGCTGTGATGATCAACGCGGATCGAGCGGTC 300
QY 524 ACAGTCATGAGCCATCAAGCAAAAGAACTAATCCAAAGGGGTGAGATGATTAATAGTT 583
DB 301 ACAGTCATGAGCCATCAAGCAAAAGAACTAATCCAAAGGGGTGAGATGATTAATAGTT 360
QY 584 TAAATATAGTTAAACAGCGGAAA- GCTGCTGACGAGCCAGGTCACTTATCTTACC 642

DB 361 TAAAAATTAGTTAAACACAGCGGAAAAGGCTGTCTGACAGCCAGGTCACTTATCTTTACC 420
QY 643 TGTGTCGAAATGATTCGTGTCTGTGATTTTAAATTTTGTGAAAGCCGGAATAA 702
DB 421 TGTGTCGAAATGATTCGTGTCTGTGATTTTAAATTTTGTGAAAGCCGGAATAA 480
QY 703 AGTTGTAAAGAGATAAACCCTATATAAATTCATATATTTCTCCCGCTTTTGAATTG 762
DB 481 AGTTGTAAAGAGATAAACCCTATATAAATTCATATATTTCTCTCCGCTTTTGAATTG 540
QY 763 TCTGTTGTCCTCCCTCACTTTTCATCAGCCGTTTGAATTCCTCCGCGACTTGACAGAGA 822
DB 541 TCTGTTGTCCTCCCTCACTTTTCATCAGCCGTTTGAATTCCTCCGCGACTTGACAGAGA 600
QY 823 AACAGGAGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGAGATTCATTTCCCTTT 882
DB 601 AACAGGAGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGAGATTCATTTCCCTTT 660
QY 883 TGAATCTTCTCAATCTCATCTTCTTCTTCTCCGCTCTTCTTCTCCAAAGTAATAGAACTT 942
DB 661 TGAATCTTCTCAATCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 717
QY 943 TCTGATCTACTTTATTTGCTGATCTCGATCTGCTTCTCAATTTCTTCTGATCTGG 1002
DB 718 TCTGATCTACTTTATTTGCTGATCTCGATCTGCTTCTCAATTTCTTCTGATCTGG 777
QY 1003 AATTCGTTTAAATTTGGATCTGTGAACCTCCACTAAATCTTTTGGTTTACTAGAACT 1062
DB 778 AATTCGTTTAAATTTGGATCTGTGAACCTCCACTAAATCTTTTGGTTTACTAGAACT 837
QY 1063 TTAAGTTACCGATCAGTTAGCTCGATTTATAGCTACAGAAATTTGGCTTGAACCTTGA 1122
DB 838 TTAAGTTACCGATCAGTTAGCTCGATTTATAGCTACAGAAATTTGGCTTGAACCTTGA 897
QY 1123 AGATCCATCTGTTCTGTTCTTCTGCTGGAATGATTTGATGATGATGATGATGAT 1182
DB 898 AGATCCATCTGTTCTGTTCTTCTGCTGGAATGATTTGATGATGATGATGATGAT 957
QY 1183 GTTCAATGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1242
DB 958 GTTCAATGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017
QY 1243 GTTCAATGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1302
DB 1018 GTTCAATGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077
QY 1303 AACAGGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGAGATTCATTTCCCTTT 1362
DB 1078 AACAGGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGAGATTCATTTCCCTTT 1137
QY 1363 TGTTCGAGCTCATAAAAAATGGCTGAGGCTGA 1395
DB 1138 TGTTCGAGCTCAGGATCCATGATGATGATGATGATGATGATGATGATGATGAT 1170
RESULT 11
ABK52080
ID ABK52080 standard; DNA; 1259 BP.
XX
AC ABK52080;
XX
DT 13-AUG-2002 (first entry)
XX
DE Modified plant promoter #5.
XX
KW Promoter; ds: plant; soybean; peanut; alfalfa; tomato; eggplant; potato;
KW cabbage; turnip; rapeseed; apple; pear; berry; cucumber; carrots;
XX transgenic plant.
OS Synthetic.
XX
FN US2002049992-A1.
XX

PD 25-APR-2002.
 XX 22-JUN-2001; 2001US-00887384.
 XX 01-DEC-1999; 99US-00453366.
 XX (HAMI/) HAMILTON C.
 XX Hamilton C;
 XX WPI; 2002-434778/45.
 XX Modified plant promoter DNA sequences, useful for expressing genes in
 PT monocot and dicotyledon plants, e.g. soybean, tomato, cabbage, apples,
 PT cucumbers, beets and carrots.
 XX Claim 1; Page 11; 18pp; English.
 XX This invention relates to novel modified plant promoters given in the
 CC specification, their complements or double stranded equivalents. The
 CC modified DNA promoters can be efficiently expressed in higher eukaryotes
 CC (e.g. plants), and used to direct gene expression within them. In
 CC particular the modified promoters are efficiently expressed in
 CC dicotyledonous plants, e.g. species of legumes from the family Fabaceae
 CC (such as soybean, peanut, and alfalfa), species of the Solanaceae family
 CC (e.g. tomato, eggplant and potato), species of the family Brassicaceae
 CC (e.g. cabbage, turnips and rapeseed), species of the family Rosaceae
 CC (e.g. apples, pears and berries), and members of the families
 CC Cucurbitaceae (e.g. cucumbers), Chenopodiaceae (e.g. beets) and
 CC Umbelliferae (e.g. carrots). Although effective, the promoters have not
 CC been modified or optimized to provide enhanced or improved
 CC characteristics or traits. The DNA plant promoters have been modified to
 CC advantageously provide improved characteristics or traits in plants and
 CC are efficiently expressed in higher eukaryotes (e.g. plants). The DNA
 CC constructs allow for the preparation of stably transformed cells
 CC expressing heterologous proteins, and for the subsequent regeneration of
 CC fertile, transgenic plants and progeny containing desired modified
 CC promoters. The present sequence represents a modified plant promoter of
 CC the invention
 XX Sequence 1259 BP; 380 A; 204 C; 246 G; 429 T; 0 U; 0 Other;
 SQ

Query Match 76.5%; Score 1104.6; DB 6; Length 1259;
 Best Local Similarity 94.0%; Pred. No. 5.6e-257;
 Matches 1198; Conservative 0; Mismatches 59; Indels 18; Gaps 4;

164 CAACATATTTTATGATCAGAGTCAGCATATGATATGATTAATTTGATTCAGAAATCGTTTGAC 223
 1 CAACATATTTTATGATCAGAGTTTCATCTTGTAATTTGATTCAGAAATCGTTTGAC 60
 224 GAGTTCGGATGTAGTAGTATGATTAATTTATGATCATACTAATCGTGAATGATGATG 283
 61 GAGTTCGGATGTAGTAGTATGATTAATTTATGATCATACTAATCGTGAATGATGATG 120
 284 ATGAACATGTATCTTATGATTAATTTATGATCATACTAATCGTGAATGATGATG 343
 121 ATGAACATGTATCTTATGATTAATTTATGATCATACTAATCGTGAATGATGATG 180
 344 TCAGGTCGTGAATTAATTTATGATCATACTAATTTATGATTAATTTATGATCATACT 403
 191 TCAGGTCGTGAATTAATTTATGATCATACTAATTTATGATTAATTTATGATCATACT 240
 404 TGTATGAATCTAATTTATGATTAATTTATGATTAATTTATGATTAATTTATGATTAAT 463
 241 TGTATGAATCTAATTTATGATTAATTTATGATTAATTTATGATTAATTTATGATTAAT 300
 464 CGGTTTAAAGTTAAACCAACCGGAGCTGATGTAACACGGGATCGACAGGTC 523
 301 AAGTTTAAAGTTAAACCAACCGGAGCTGATGTAACACGGGATCGACAGGTC 360
 524 ACAGTCATGAAGCCATCAAGCAAAAGAACTAATCCAGGGGTGAGATGATTAATTTAGTT 583
 361 ACAGTCATGAAGCCATCAAGCAAAAGAACTAATCCAGGGGTGAGATGATTAATTTAGTT 420

QY 584 TAAAAATTTAGTTAAACACGAGGGAAR-GCTGTCTGACAGCCAGGTACGTTATCTTTACC 642
 Db 421 TAAAAATTTAGTTAAACACGAGGGAAR-GCTGTCTGACAGCCAGGTACGTTATCTTTACC 480
 QY 643 TGTGTCGAAATGATTCGTGTCTGTGATTTTAAATTTTGTGAAAGCCGAAATAA 702
 Db 481 TGTGTCGAAATGATTCGTGTCTGTGATTTTAAATTTTGTGAAAGCCGAAATAA 540
 QY 703 AGTTGTAGAGATAAACCCGCTATATAATTCATATATTTCTCTCCCGCTTTGAATG 762
 Db 541 AGTTGTAGAGATAAACCCGCTATATAATTCATATATTTCTCTCCCGCTTTGAATG 600
 QY 763 TCTGTTGTCT 822
 Db 601 TCTGTTGTCT 660
 QY 823 AACAGGAAGAAGATTAAGAGAAAGTAAGAGATAATCCAGGATTCATCTCCGTTT 882
 Db 661 AACAGGAAG-----AGAGAGAAAGTAAGAGATAATCCAGG-----TTCTCCGTTT 706
 QY 883 TGAATCT 942
 Db 707 TGAATCT 763
 QY 943 TCTGATCT 1002
 Db 764 TCTGATCT 823
 QY 1003 AATTCGTTTAAATTTGATCTGTGAACTCCCAATAATCTTTGCTTTTACTAGAAATCGAT 1062
 Db 824 TTTTCGTTTAAATTTGATGGAATTTAGATCACTAAATCTTTGGTTTACTAGAAATCGAT 883
 QY 1063 CTAGTTGACCGATCAGTTAGTCGATTAATAGTATAGTATAGTATAGTATAGTATAGTAT 1122
 Db 884 CTAGTTGACCGATCAGTTAGTCGATTAATAGTATAGTATAGTATAGTATAGTATAGTAT 943
 QY 1123 AGAGATCCATGTTTACCTGGGAAATGATTTGTATATGTAATTTGAAATCTGAACT 1182
 Db 944 AGAGATCCATGTTTACCTGGGAAATGATTTGTATATGTAATTTGAAATCTGAACT 1003
 QY 1183 GTTGAAGTTAGATTAATGAACTGAACTGCAATGATTTAGATTTAGATTTAGATTTAGATTT 1242
 Db 1004 GTTGAAGTTAGATTAATGAACTGAACTGCAATGATTTAGATTTAGATTTAGATTTAGATTT 1063
 QY 1243 GTTGAAGTTAGATTAATGAACTGAACTGCAATGATTTAGATTTAGATTTAGATTTAGATTT 1302
 Db 1064 GTTGAAGTTAGATTAATGAACTGAACTGCAATGATTTAGATTTAGATTTAGATTTAGATTT 1123
 QY 1303 AACAGAAAGCTATTTCTGATTAATCAATCAGGTTTATTTGATTTGATTTGATTTGATTTG 1362
 Db 1124 AACAGAAAGCTATTTCTGATTAATCAATCAGGTTTATTTGATTTGATTTGATTTGATTTG 1183
 QY 1363 TGTGTCGAGCTATTAATAAATGCGTGGAGCTGACCAATTAATCAATCAATCAATCAATCAAT 1422
 Db 1184 TGTGTCGAGCTATTAATAAATGCGTGGAGCTGACCAATTAATCAATCAATCAATCAATCAAT 1243
 QY 1423 TGTGTCGAGCTATTAATAAATGCGTGGAGCTGACCAATTAATCAATCAATCAATCAATCAAT 1437
 Db 1244 TGTGTCGAGCTATTAATAAATGCGTGGAGCTGACCAATTAATCAATCAATCAATCAATCAAT 1258

RESULT 12

AAD01288

ID AAD01288 standard; DNA; 15676 BP.

XX AAD01288;

XX 12-OCT-2000 (first entry)

XX Arabidopsis transformation binary vector, pAct2-bin.

XX Matrix Attachment Region; MAR; scaffold attachment region;

KW


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FT      /tag= a
FT      /note= "Corresponds to nucleotides 1-646 of MAR dimer-1"
FT      misc_feature
FT      4044..4689
FT      /tag= b
FT      /note= "Corresponds to nucleotides 1-646 of MAR dimer-3"
XX
XX      WO200032800-A1.
XX
XX      08-JUN-2000.
XX
XX      30-NOV-1999; 99WO-US028123.
XX
XX      01-DEC-1998; 98US-0110437P.
XX
XX      (DOMC ) DOM AGROSCIENCES LLC.
XX
XX      Van Der Geest AHM, Ainley WM, Cowen NM, Weiler ME, Woosley AT;
XX      WPI; 2000-412345/35.
XX
XX      An isolated DNA molecule for use as a matrix attachment region to
XX      increase expression of genes introduced in transformed plants comprises a
XX      298 base pair sequence described in the specification.
XX
XX      Example 3; Page 64-68; 73pp; English.
XX
XX      The patent discloses a DNA molecule, useful as matrix attachment region
XX      (MAR) or scaffold attachment region, to increase the expression of genes
XX      introduced in transformed plants. MARs are located in non-transcribed
XX      regions of genes and form the physical boundaries of individual DNA
XX      loops. They are rich in adenosine and thymine bases and contain certain
XX      conserved sequence elements and structural features. They are about 300-
XX      2000 bp in length. Increased levels of expression of DNA introduced into
XX      cells can be achieved by use of MAR. They can also reduce the position
XX      effect in transgenic organisms. The present DNA sequence is the
XX      Arabidopsis transformation binary vector pFAct2Af-bin, identical to the
XX      vector pAct2-bin, except that it contains a MAR dimer-1 positioned 5' to
XX      the Act2 transcription initiation region and the MAR dimer-3 positioned
XX      3' to the nos 3' UTR (untranslated region). This vector is used to test
XX      the two orientations of the artificial MAR dimer in Arabidopsis
XX
XX      Sequence 17116 BP; 4686 A; 3968 C; 4052 G; 4407 T; 0 U; 3 Other;
XX
XX      Query Match      74.7%; Score 1078.8; DB 3; Length 17116;
XX      Best Local Similarity 98.3%; Pred. No. 2.2e-250;
XX      Matches 1154; Conservative 0; Mismatches 12; Indels 8; Gaps 6;
XX
XX      205 GATTCAAGATCGTTTGGACGATTCGGATGTAGTAGTAGCCATTATTTAATGTACATACT 264
XX      718 GAATTCGGCTTGTGTTGACGAGTTCGGATGTAGTAGTAGCCATTATTTAATGTACATACT 777
XX
XX      265 AATCGTGAATAGTG-ATATGATGAACATGTATCTTATTTGATTAATATCCATAACAC 323
XX      778 AATCGTGAATAGTGAAATATGATGAACATGTATCTTATTTGATTAATATCCATAACAC 837
XX
XX      324 ATCATGAAGACACATTTCTTTTCAGGCTCTGAATTAATATGACACAAATTTCTAATAGAAA 383
XX      838 ATCATGAAGACACATTTCTTTTCAGGCTCTGAATTAATATGACACAAATTTCTAATAGAAA 897
XX
XX      384 CGAATTAATATAGTTGAATGTATGAATCTAATTAATGAACCAACCAACGAGGAGAC 443
XX      898 CGAATTAATATAGTTGAATGTATGAATCTAATTAATGAACCAACCAACGAGGAGAC 957
XX      444 TAACTGTTGCTGATGACTCGGTTTAAGTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 503
XX      958 TAACTGTTGCTGATGACTCGGTTTAAGTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1017
XX      504 ACACGCGGATCGGAGGAGTTCACAGTCATGAAGCCATCAAAAGCAAAAGAACTAATCCAAAG 563
XX      1018 ACACGCGGATCGGAGGAGTTCACAGTCATGAAGCCATCAAAAGCAAAAGAACTAATCCAAAG 1077
XX      564 GG-TGAGATGAATTAATAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 621

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Db      1078 GGCTGAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1137
Qy      622 CCAGGTCAAGTATATCTTTACCTGTGTGCGAATGATTCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 581
Db      1138 CCAGGTCAAGTATATCTTTACCTGTGTGCGAATGATTCGTGTGTGTGTGTGTGTGTGTGTGTGT 1197
Qy      682 TTTTGTGAAGGCGCGAATAAAGTTGTAAGAGATAAACCCTTATATATAATTCATATAT 741
Db      1198 TTTTGTGAAGGCGCGAATAAAGTTGTAAGAGATAAACCCTTATATATAATTCATATAT 1257
Qy      742 TTTTCTCCCGGTTTGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 801
Db      1258 TTTTCTCTCGGTTTGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1317
Qy      802 TCCGCGGACTTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 861
Db      1318 TCCGCGGACTTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1377
Qy      862 CAGGAGATTCATCTCCGTTTGAATCTTCTCAATCTCATCTTCTTCTCGGCTCTTCTT 921
Db      1378 CAGGAGATTCATCTCCGTTTGAATCTTCTCAATCTCA--TCTTCTCGGCTCTTCTT 1434
Qy      922 TTTCCAGGTAATAGAGAACTTTCTGGATCTTCTTATTTGCTGGATCTCGATCTTGTGTTT 981
Db      1435 TTTCCAGGTAATAGAGAACTTTCTGGATCTTCTTATTTGCTGGATCTCGATCTTGTGTTT 1494
Qy      982 CTCATTTCTCGGATCTGGAATCTGTTTAAATTT--GGATCTGTGAACCTCCACTTAAATC 1040
Db      1495 CTCATTTCTCGGATCTGGAATCTGTTTAAATTTGGAATCTGTGAACCTCCACTTAAATC 1554
Qy      1041 TTTTGGTTTCTAGAACTGATCTAAGTTGACCGATCAGTTAGTCTCGATTTAGTACCA 1100
Db      1555 TTTTGGTTTCTAGAACTGATCTAAGTTGACCGATCAGTTAGTCTCGATTTAGTACCA 1614
Qy      1101 GAATTCGGCTGACCTGATGAGAGAGATCCATGTTCAATGTTTACTCGGAAATGATTTGTA 1160
Db      1615 GAATTCGGCTGACCTGATGAGAGATCCATGTTCAATGTTTACTCGGAAATGATTTGTA 1674
Qy      1161 TATGTGAATTAAGAACTCAACTGTGAAGTTAGTTGAATCTGAACACATGTCATGTTAG 1220
Db      1675 TATGTGAATTAAGAACTCAACTGTGAAGTTAGTTGAATCTGAACACATGTCATGTTAG 1734
Qy      1221 ATGTAATCTGAACACATGTTTAA--GTTAGATGAAGTTGTGTATAGATTCTTCGAAACCTT 1279
Db      1735 ATGTAATCTGAACACATGTTTAAAGTTAGATGAAGTTGTGTATAGATTCTTCGAAACCTT 1794
Qy      1280 AGGATTTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1339
Db      1795 AGGATTTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1854
Qy      1340 GACTGTATTGAACCTCTTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1373
Db      1855 GACTGTATTGAACCTCTTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1888
XX
XX      RESULT 15
XX      ABKS2077
XX      ID ABKS2077 standard; DNA; 1202 BP.
XX
XX      AC ABKS2077;
XX
XX      DT 13-AUG-2002 (first entry)
XX
XX      DE Modified plant promoter #2.
XX
XX      KW Promoter; ss; plant; soybean; peanut; alfalfa; tomato; eggplant; potato;
XX      cabbage; turnip; rapeseed; apple; pear; berry; cucumber; carrots;
XX      transgenic plant.
XX
XX      OS Synthetic.
XX
XX      PN US2002049992-A1.
XX
XX

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1174.8	81.4	1219	4	US-09-737-6988-9	Sequence 9, Appli
2	1174.8	81.4	1219	4	US-09-737-626A-9	Sequence 9, Appli
3	1174	81.3	1742	4	US-09-737-698B-30	Sequence 30, Appl
4	1174	81.3	1742	4	US-09-737-626A-30	Sequence 30, Appl
5	75.4	5.2	1271	4	US-09-737-698B-10	Sequence 10, Appl
6	75.4	5.2	1271	4	US-09-737-626A-10	Sequence 10, Appl
7	73.8	5.1	1800	4	US-09-737-698B-29	Sequence 29, Appl
8	73.8	5.1	1800	4	US-09-737-626A-29	Sequence 29, Appl
9	50.4	3.5	6070	4	US-10-204-708-9	Sequence 9, Appli
10	48.6	3.4	731	1	US-08-451-405A-2	Sequence 2, Appli
11	47.8	3.3	5203	4	US-09-257-770-1	Sequence 1, Appli
12	46.6	3.2	6406B1	4	US-09-790-388-1	Sequence 1, Appli
13	46.2	3.2	2448	1	US-08-526-964-2	Sequence 2, Appli
14	46.2	3.2	2448	2	US-09-946-617-2	Sequence 2, Appli
15	46.2	3.2	2448	3	US-09-031-997-2	Sequence 2, Appli
16	45.4	3.1	7218	1	US-08-232-463-14	Sequence 14, Appl
17	45.2	3.1	1705	1	US-08-090-523-25	Sequence 25, Appl
18	45.2	3.1	1705	1	US-08-334-639-4	Sequence 4, Appli
19	45.2	3.1	1705	1	US-08-398-627-25	Sequence 25, Appl
20	45.2	3.1	1705	1	US-08-406-458-26	Sequence 26, Appl
21	45.2	3.1	1705	4	US-08-399-023-25	Sequence 25, Appl
22	45.2	3.1	1705	5	PCT-US94-05275-26	Sequence 26, Appl
23	44.4	3.1	7218	1	US-08-232-463-14	Sequence 14, Appl
24	43.4	3.0	287	4	US-09-313-294A-6702	Sequence 6702, Ap
25	42.8	3.0	274	4	US-09-313-294A-2611	Sequence 2611, Ap
26	42.6	3.0	774	4	US-09-134-001C-725	Sequence 725, App
27	42.4	2.9	288	4	US-09-313-294A-4386	Sequence 4386, Ap

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; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/09/737,626A
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 9
; LENGTH: 1219
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1219)
; OTHER INFORMATION: Act2 promoter polynucleotide sequence and intron
US-09-737-626A-9

301 CGGTTAAGTTAAACCACTTAAACCAAGGAGCTGTATGTAACACCGGATCGAGCGGTC 360
524 ACAGTCATGAAGCCATCAAGCAAGAACTAAATCCAGGGGTGAGATGATTAATAGTT 583
361 ACAGTCATGAAGCCATCAAGCAAGAACTAAATCCAGGGGTGAGATGATTAATAGTT 420
584 TAAATATTAGTTAAGCAAGGAAAC-CCTGCTGTGACAGCGAGCTCAAGTTATCTTACC 642
421 TAAATATTAGTTAAGCAAGGAAAGGCTGTGACAGCGAGGTCAGTTATCTTACC 480
643 TGTGGTCGAATGATTCGTGCTGCGATTTTAAATATTATTTTGAAGGCCGAAATAA 702
481 TGTGGTCGAATGATTCGTGCTGCGATTTTAAATATTATTTTGAAGGCCGAAATAA 540
703 AGTTGTAAGAGATAAACCAGGCTTATATAATTCATATTTTCTCCCGCTTGAATG 762
541 AGTTGTAAGAGATAAACCAGGCTTATATAATTCATATTTTCTCCCGCTTGAATG 600
763 TCTCGTTGCTCCTCCTCACTTTCATCAGCGGCTTTTGAATCTCCGCGACTTGACAGAGA 822
601 TCTCGTTGCTCCTCCTCACTTTCATCAGCGGCTTTTGAATCTCCGCGACTTGACAGAGA 660
823 AACAGGAAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTCTCGTT 882
661 AACAGGAAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTCTCGTT 720
883 TGAATCTTCTCAATCTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 942
721 TGAATCTTCTCAATCTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 777
943 TCTGGATCTACTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1002
778 TCTGGATCTACTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837
1003 AATTCGTTTAAATTTGGATCTGTGAACCTCCACTAAATCTTTTGGTTTACTAGAAATCGAT 1062
838 AATTCGTTTAAATTTGGATCTGTGAACCTCCACTAAATCTTTTGGTTTACTAGAAATCGAT 897
1063 CTAGTTGACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1122
898 CTAGTTGACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 957
1123 AGAGATCCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1182
958 AGAGATCCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1017
1183 GTTGAAGTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1242
1016 GTTGAAGTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1077
1243 GTTGAAGTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1302
1078 GTTGAAGTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1137
1303 AACAGAAAGCTATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1362
1138 AACAGAAAGCTATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197
1363 TGTGTCAGCTCATAAATATG 1384
1198 TGTGTCAGCTCATCAATG 1219

```

RESULT 2

```

US-09-737-626A-9
; Sequence 9, Application US/09737626A
; Patent No. 6660911
; GENERAL INFORMATION:
; APPLICANT: Finner, Karen
; APPLICANT: Flisinski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6660911el Plant Expression Constructs

```

```

Query Match 81.4%; Score 1174.8; DB 4; Length 1219;
Best Local Similarity 98.7%; Pred. No. 8.1e-306;
Matches 1206; Conservative 0; Mismatches 12; Indels 4; Gaps 2;

Qy 164 CAACATATTTTATGCTATGCAAGAGTCAGCATATGTAATAATGATTGATTCAGATCGTTTGGAC 223
Db 1 CAACATATTTTATGCTATGCAAGAGTCAGCATATGTAATAATGATTGATTCAGATCGTTTGGAC 60
Qy 224 GAGTTCGGATGTAGTAGTACCATTTATTTAATGTACATACATAATCGTGAATAGTATG 283
Db 61 GAGTTCGGATGTAGTAGTACCATTTATTTAATGTACATACATAATCGTGAATAGTATG 120
Qy 284 ATGAACATGTTATCTTATTTGTAATAATTCATAACATCATCATGTAAGACATTTCTT 343
Db 121 ATGAACATGTTATCTTATTTGTAATAATTCATAACATCATCATGTAAGACATTTCTT 180
Qy 344 TCAGGCTCGAATTAATTAATGATACAAATCTAATAGAAAACGAATTTAAATTAACCTTGAAT 403
Db 181 TCAGGCTCGAATTAATTAATGATACAAATCTAATAGAAAACGAATTTAAATTAACCTTGAAT 240
Qy 404 TGTATGAAATCTAATTTGAACAAGCCAAACACGACGAGGACTAACGTTGCTGCTGATGACT 463
Db 241 TGTATGAAATCTAATTTGAACAAGCCAAACACGACGAGGACTAACGTTGCTGCTGATGACT 300
Qy 464 CGGTTTAAAGTTAAACCACTTAAACCAAGCAAGGAGCTCATGTAAACACGCGATCGACGAGTC 523
Db 301 CGGTTTAAAGTTAAACCACTTAAACCAAGCAAGGAGCTCATGTAAACACGCGATCGACGAGTC 360
Qy 524 ACAGTCATGAGCAATCAAGCAAGAAAGAACTAAATCCAGGGGTGAGATGATTAATAGTT 583
Db 361 ACAGTCATGAGCAATCAAGCAAGAAAGAACTAAATCCAGGGGTGAGATGATTAATAGTT 420
Qy 584 TAAATATTAGTTAACAACGAGGAAAC - GCTGCTGTGACAGCGAGTCAAGTTATCTTTACC 642
Db 421 TAAATATTAGTTAACAACGAGGAAAGGCTGTGACAGCGAGTCAAGTTATCTTTACC 480
Qy 643 TGTGGTCGAATGATTCGTGCTGCGATTTTAAATATTATTTTGAAGGCCGAAATAA 702
Db 481 TGTGGTCGAATGATTCGTGCTGCGATTTTAAATATTATTTTGAAGGCCGAAATAA 540
Qy 703 AGTTGTAAGAGATAAACCAGGCTTATATAATTCATATTTTCTCCCGCTTGAATG 762
Db 541 AGTTGTAAGAGATAAACCAGGCTTATATAATTCATATTTTCTCCCGCTTGAATG 600
Qy 763 TCTCGTTGCTCCTCCTCACTTTCATCAGCGGCTTTTGAATCTCCGCGACTTGACAGAGA 822
Db 601 TCTCGTTGCTCCTCCTCACTTTCATCAGCGGCTTTTGAATCTCCGCGACTTGACAGAGA 660
Qy 823 AACAGGAAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTCTCGTT 882
Db 661 AACAGGAAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTCTCGTT 720
Qy 883 TGAATCTTCTCAATCTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 942
Db 721 TGAATCTTCTCAATCTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 777

```


RESULT 4

US-09-737-626A-30
 ; Sequence 30, Application US/09737626A
 ; Patent No. 6660911
 ; GENERAL INFORMATION:
 ; APPLICANT: Fincher, Karen
 ; APPLICANT: Flaslinski, Stanislaw
 ; APPLICANT: Wilkinson, Jack
 ; TITLE OF INVENTION: No. 6660911el Plant Expression Constructs
 ; FILE REFERENCE: 38-21(51499)B
 ; CURRENT APPLICATION NUMBER: US/09/737,626A
 ; CURRENT FILING DATE: 2002-02-25
 ; PRIOR APPLICATION NUMBER: 09/737,626
 ; PRIOR FILING DATE: 2000-12-15
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 30
 ; LENGTH: 1742
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; NAME/KEY: promoter
 ; LOCATION: (1)..(1742)
 ; OTHER INFORMATION: chimeric promoter fusion CamV and Act2 polynucleotides + Act2 in
 ; OTHER INFORMATION: tro
 ; US-09-737-626A-30

Query Match 81.3%; Score 1174; DB 4; Length 1742;
 Best Local Similarity 99.3%; Pred. No. 1.5e-305;
 Matches 1201; Conservative 0; Mismatches 5; Indels 4; Gaps 2;
 QY 164 CAACATATTTTATGATGACGAGTTCAGCATATGATTAATGATTCAGTTCAGTTCGTTGAC 223
 DB 533 CAACATATTTTATGATGACGAGTTCAGCATATGATTAATGATTCAGTTCAGTTCGTTGAC 592
 QY 224 GAGTTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 283
 DB 593 GAGTTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 652
 QY 284 ATGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 343
 DB 653 ATGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 712
 QY 344 TCAGGCTGGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 403
 DB 713 TCAGGCTGGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 772
 QY 404 TGATGAAATCTAATGAAAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 463
 DB 773 TGATGAAATCTAATGAAAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 832
 QY 464 CGTTTAAGTTAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 523
 DB 833 CGTTTAAGTTAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 892
 QY 524 ACAGTATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 583
 DB 893 ACAGTATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 952
 QY 584 TAAATAATGATTAACACGAGGAAAA-GCTGTCTGACAGCCAGGTCACGTTATCTTTTACC 642
 DB 953 TAAATAATGATTAACACGAGGAAAAAGGCTGTCTGACAGCCAGGTCACGTTATCTTTTACC 1012
 QY 643 TGTGCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 702
 DB 1013 TGTGCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1072
 QY 703 AGTTGTAAGAGATTAACCCGCTATATAAATTCATATATTTTCTCCCGCTTTGAATTG 762
 DB 1073 AGTTGTAAGAGATTAACCCGCTATATAAATTCATATATTTTCTCCCGCTTTGAATTG 1132

QY 763 TCTGTTGCTCTCTCACTTTTCATCAGCGTGTGTTGAATCTCCGGGACCTTCACAGAGAAG 822
 DB 1133 TCTGTTGCTCTCTCACTTTTCATCAGCGTGTGTTGAATCTCCGGGACCTTCACAGAGAAG 1192
 QY 823 AACAGGAAGAGACTAAG 882
 DB 1193 AACAGGAAGAGACTAAG 1252
 QY 883 TGAATCTTCTCAATCTCAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 942
 DB 1253 TGAATCTTCTCAATCTCAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1309
 QY 943 TCTGGATCTACTTTTATTTGCTGGATCTCGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1002
 DB 1310 TCTGGATCTACTTTTATTTGCTGGATCTCGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1369
 QY 1003 AATTCGTTTAAATTCGATCTGTGAACCTCCACTAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1062
 DB 1370 AATTCGTTTAAATTCGATCTGTGAACCTCCACTAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1429
 QY 1063 CTAAGTTGACCGATCAGTTAGCTCGATTTAGCTTACAGAAATTTGGCTTGACCTTGATGG 1122
 DB 1430 CTAAGTTGACCGATCAGTTAGCTCGATTTAGCTTACAGAAATTTGGCTTGACCTTGATGG 1489
 QY 1123 AGAGATCCATGTTTATGTTTACCTGGGAATGATTTGATATATGATGATGATGATGATGATGATG 1182
 DB 1490 AGAGATCCATGTTTATGTTTACCTGGGAATGATTTGATATATGATGATGATGATGATGATGATG 1549
 QY 1193 GTTGAAGTTAGATTCAGTTCGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1242
 DB 1550 GTTGAAGTTAGATTCAGTTCGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1609
 QY 1243 GTTGAAGTTAGATTCGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1302
 DB 1610 GTTGAAGTTAGATTCGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1669
 QY 1303 AACAGAAAGCTATTTCTGATTCATCAATCAGGGTTTATGATGATGATGATGATGATGATGATGATG 1362
 DB 1670 AACAGAAAGCTATTTCTGATTCATCAATCAGGGTTTATGATGATGATGATGATGATGATGATGATG 1729
 QY 1363 TGTGTCGAGC 1372
 DB 1730 TGTGTCGAGC 1739

RESULT 5

US-09-737-698B-10
 ; Sequence 10, Application US/09737698B
 ; Patent No. 6462258
 ; GENERAL INFORMATION:
 ; APPLICANT: Fincher, Karen
 ; APPLICANT: Wilkinson, Jack
 ; TITLE OF INVENTION: No. 6462258el Plant Expression Constructs
 ; FILE REFERENCE: 38-21(51499)C
 ; CURRENT APPLICATION NUMBER: US/09/737,698B
 ; CURRENT FILING DATE: 2000-12-15
 ; PRIOR APPLICATION NUMBER: US 60/171,173
 ; PRIOR FILING DATE: 1999-12-16
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 1271
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; NAME/KEY: promoter
 ; LOCATION: (1)..(1271)
 ; OTHER INFORMATION: y = t/u or c
 ; OTHER INFORMATION: Act8 promoter polynucleotide sequence and intron
 ; US-09-737-698B-10

Query Match 5.2%; Score 75.4; DB 4; Length 1271;
 Best Local Similarity 51.6%; Pred. No. 1.2e-10;

QY 962 CTGGATCTCGATCTGTGTTCTCAATTTCTTGGATCTGGAATCTGTTAAATTT 1016
 |||||
 Db 1364 TTGGATCTCGATTACGATTTCTAAGTTACCTTCAAAAGTTGTTCCGATTTGATT 1418
 |||||

RESULT 8

US-09-737-626A-29
 ; Sequence 29, Application US/09737626A
 ; Patent No. 6660911
 ; GENERAL INFORMATION:
 ; APPLICANT: Fincher, Karen
 ; APPLICANT: Flasiński, Stanisław
 ; APPLICANT: Wilkinson, Jack
 ; TITLE OF INVENTION: No. 6660911el Plant Expression Constructs
 ; FILE REFERENCE: 38-21(51499)B
 ; CURRENT APPLICATION NUMBER: US/09/737,626A
 ; CURRENT FILING DATE: 2002-02-25
 ; PRIOR APPLICATION NUMBER: 09/737,626
 ; PRIOR FILING DATE: 2000-12-15
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 29
 ; LENGTH: 1800
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; NAME/KEY: promoter
 ; LOCATION: (1)..(1800)
 ; OTHER INFORMATION: y = t/u or c
 ; OTHER INFORMATION: chimeric promoter fusion CamV and Act8 polynucleotides + Act8 in
 ; OTHER INFORMATION: ttc
 US-09-737-626A-29

Query Match 5.1%; Score 73.8; DB 4; Length 1800;
 Best Local Similarity 51.3%; Pred. No. 3.7e-10;
 Matches 213; Conservative 3; Mismatches 195; Indels 4; Gaps 2;
 QY 606 AAAAGCTGTCGACAGCCAGTCACGTTA---TCTTTTACCTGGTGGTGAATGATTCGG 662
 |||||
 Db 1004 AGAGGCTGCTGACAGCCAGTCACGTTATTTTCCGTATGATCGAATGATTCGTC 1063
 |||||
 QY 663 TCTGTCGATTTAATTTATTTTGAAGCGGAAAAATAAGTTGTAAGAGATAAACCCG 722
 |||||
 Db 1064 TTGGYGAATTTAATTTTCCAAATTTGACCTTAAGAAAGAAAATAGTTTTC 1123
 |||||
 QY 723 CCAATATAAATCAATATTTCTCCCGCTTTGAAATGCTCGGTGCTCTCTCACTT 782
 |||||
 Db 1124 GATAAACCCGCTATATAAATAGTTCAACACTCGGTTTATTTCTTCTCCCTCAAAGAA 1183
 |||||
 QY 783 TCATCAGCCGTTTGAATCTCCGCGACTTGACAGAGAAGAACAGGAAGACTAAGA 842
 |||||
 Db 1184 TGGCTGCTGCTTCAGCTTCATCGCCGCTTGCAATTTCCCGCGATTAAGAGAGAAAG 1243
 |||||
 QY 843 -GAGAAAGTAAGAGATAATCCAGAGATTCATTTCCGTTTGAATCTCTCAATCTCA 901
 |||||
 Db 1244 GGAGAAAGAGTGAGCCAGATCTTCATCGTCGGTGTCTGTTCTTCTCTCGATCTCTCGA 1303
 |||||
 QY 902 TCTTCTCTTCGCTCTTTCTTCTCCAGGTAATAGGAATCTTCGATCTACTTTATTG 961
 |||||
 Db 1304 TCTTCTGCTTTTGTCTTCCGATTAAGGTAATTAACCCCTCCGATCTACTTGTCTGTG 1363
 |||||
 QY 962 CTGGATCTCGATCTGTTTCTCAATTTCTTGGATCTCGAATCTGTTAAATTT 1016
 |||||
 Db 1364 TTGAATCTGATTAAGATTTCTAAGTTACCTTCAAAAGTTGTTCCGATTTGATT 1418
 |||||

RESULT 9

US-10-204-708-9
 ; Sequence 9, Application US/10204708
 ; Patent No. 6677731
 ; GENERAL INFORMATION:
 ; APPLICANT: OLEK, Alexander
 ; APPLICANT: PIEPENBROCK, Christian

; APPLICANT: BERLIN, Kurt
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
 ; TITLE OF INVENTION: By Assessing DNA Methylation
 ; FILE REFERENCE: 5013.1012
 ; CURRENT APPLICATION NUMBER: US/10/204,708
 ; CURRENT FILING DATE: 2003-05-06
 ; PRIOR APPLICATION NUMBER: PCT/EP01/03971
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: DE 10019058.8
 ; PRIOR FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: DE 10019173.8
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: DE 10032529.7
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: DE 10043826.1
 ; PRIOR FILING DATE: 2000-09-01
 ; NUMBER OF SEQ ID NOS: 98
 ; SEQ ID NO 9
 ; LENGTH: 6070
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 US-10-204-708-9

Query Match 3.5%; Score 50.4; DB 4; Length 6070;
 Best Local Similarity 44.9%; Pred. No. 0.0012;
 Matches 192; Conservative 0; Mismatches 236; Indels 0; Gaps 0;
 QY 838 TAAGAGAGAAAGTAAGAGATAATCCAGGAGATCAATTCCTCGTTTGAATCTTCCCTCAAT 897
 |||||
 Db 3589 TAGTAGAGATTCGATGTTTAAAGTCGTTGATTATTTATATTTTATTAATTTATTTAT 3648
 |||||
 QY 898 CTGATCTCTTCTCCGCTCTTCTTCCAGGTAATAGCAACTTCTCGATCTACTTTA 957
 |||||
 Db 3649 GAGAGTTTATTTTGTATTTTGTAAATTAAGGAATTTGTTATTTTATTTAGTTA 3708
 |||||
 QY 958 TTTCTCGATCTCGATCTGTTTCTCAATTTCTTGAGATCTGGAATTCGTTTAAATTTG 1017
 |||||
 Db 3709 TTTTATGAGTGTGTTAAATAGTATTTATTTTGGTTTAAATTTATTAAGAAGATTTT 3768
 |||||
 QY 1018 GATCTGTGAACCTCCATTAATCTTTGTTTACTAGATCGATCTAAGTTGACCGATC 1077
 |||||
 Db 3769 GAGGAGGTAATTCGAATAGATTTTATATTTTAAAGAAATTTTTCGATTTATCTGG 3828
 |||||
 QY 1078 AGTTAGCTCGATTATAGTACCAGATTTGCTTGACCTTGATGAGAGATCCCATGTCA 1137
 |||||
 Db 3829 AGAATGATTTATTTGTAATTAAGTTTATAGTATTTATTTATTAATAGTTAAAGGTG 3888
 |||||
 QY 1138 TGTACCTCGGAATGATTTGTATATGTAATCTGAATCTGAATCTGAACTGTTGAAGTTAG 1197
 |||||
 Db 3889 GAATAATTAAGTATTTATTTATATGGAATGAATGAATAAATAAATAGTATATATGAT 3948
 |||||
 QY 1198 AATCTGAACACTGTCATGTTAGATTTGAATCTGAACACTGTTTAAAGTTAGTGAAGTTG 1257
 |||||
 Db 3949 AATGGAATATTTATTTAGTTTAAAGAGGAAGAAATTTTGATATATATGTTATATATAG 4008
 |||||
 QY 1258 TGTATAGA 1265
 |||||
 Db 4009 TTTTITGA 4016
 |||||

RESULT 10

US-08-451-405A-2/c
 ; Sequence 2, Application US/08451405A
 ; Patent No. 5736358
 ; GENERAL INFORMATION:
 ; APPLICANT: FASEL, NICOLAS JOSEPH
 ; APPLICANT: KEYMOND, CHRISTOPHE DOMINIQUE
 ; TITLE OF INVENTION: DICTYOSTELID EXPRESSION VECTOR AND
 ; TITLE OF INVENTION: METHOD FOR EXPRESSING A DESIRED PROTEIN
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: THE WEBB LAW FIRM
STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
CITY: PITTSBURGH

STATE: PENNSYLVANIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 15219-1818

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" FLOPPY DISK

COMPUTER: Midwest Micro 486-50

OPERATING SYSTEM: DOS

SOFTWARE: WORDPERFECT 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/451,405A

FILING DATE: 26-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/965,273

FILING DATE: 15-JAN-1993

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 731

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

TOPOLOGY: UNKNOWN

US-08-451-405A-2

Query Match 3.4%; Score 48.6; DB 1; Length 731;

Best Local Similarity 49.0%; Pred. No. 0.0014;

Matches 129; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 168 TATTTTATGATGCAAGAGTCAGCATATGTAATTAATTCAGATCGTTTCAGCAGT 227

DB 698 TTTTITTTTAAAGAAAAAATAAATTTTGAATGATTAAGAAAAAATAAATAAAT 639

QY 228 TCGAGTAGTAGTACCATTAATTAATGTCATACACTAATCGTGAATAGTATGATGA 287

DB 638 AATAATGTAAGAAAAAGTATTTTATTAAGAAAAAATTAATTAATTAATTAAGAAAA 579

QY 288 AACATCTATCTATTGTATATAATCCATAACACATCATGAAGACACTTTCTTCAG 347

DB 578 TATTTTATTTCTAATGATATATAATAATAATAATAATAATAATAATAATAATA 519

QY 348 GGTCTGAATTAATTAATGATACAAATCTTAATGAGAAACGAATTAATTAATGTA 407

DB 518 TAAAGGGTGTGCTGTAAGAAAAAATAAATAATAATAATAATAATAATAATAATA 459

QY 408 TGAATCTAATTAAGCAAGCCAA 430

DB 458 AAAATAATAATAATAATAAAAAA 436

RESULT 11

US-09-257-770-1/c

Sequence 1, Application US/09257770

Patent No. 6306596

GENERAL INFORMATION:

APPLICANT: Lambowitz, Allen M.

APPLICANT: Zimmerly, Steven

APPLICANT: Guo, Huatao

APPLICANT: Mohr, Georg

APPLICANT: Beall, Clifford J.

TITLE OF INVENTION: Methods for Cleaving Single-Stranded and

DOUBLE-STRANDED DNA SUBSTRATES WITH NUCLEOTIDE

TITLE OF INVENTION: Integrase

FILE REFERENCE: 24671/04007

CURRENT APPLICATION NUMBER: US/09/257,770

CURRENT FILING DATE: 1999-02-25

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 1

LENGTH: 5203

TYPE: DNA

ORGANISM: S. cerevisiae

US-09-257-770-1

Query Match 3.3%; Score 47.8; DB 4; Length 5203;

Best Local Similarity 45.8%; Pred. No. 0.0056;

Matches 160; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 73 AATATGNNACGACAAATGGCTACACTCGATGTAATGGTATCTCAACTCAACATTATAC 132

DB 2378 AATATACCTCTATGTAATTTGTTTAAACATGATGATTTCTCATCAATAGTTGAATTA 2319

QY 133 TTATACCAACATTAAGTAGCAAAATTTAAACAACATATTTTATGATCGACAGAGTCAGC 192

DB 2318 ATACTACAGGTTTATTAATAATTTAGCTTTAGCTGAGTAATATATATTAATTAATG 2259

QY 193 ATATGATATTAATTCAGAAATCGTTTTCAGCAGTTTCGAGTAGTAGTAGCCATTATTT 252

DB 2258 ATATATTTCAAAAGGATCAGTTACTTTAGCTTCTGATATATATAATAATATACCAT 2199

QY 253 AATGTACATACATACTAATCGTAATAGTATGATGAACATTTGTTTATTTGTAATAATA 312

DB 2198 TCAATTTTGTGATATATCAAAAGTATTTCTTGMAAATTTGCAATTAATTTATCATTT 2139

QY 313 TCCATAAACACATCATGAAGACACACTTTCTTTTCAGGGTCTGCAATTAATTTATGATCA 372

DB 2138 TCAATAATATTTAAATTTATAACCAAAATTTTAAATAGTTTACTTAATGTTTAAATCTA 2079

QY 373 CTAATAGAAACGAATTAATTAATTCAGTTGTAATGTAATAATCTAATTTGA 421

DB 2078 TATTTACTAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2030

RESULT 12

US-09-790-988-1

Sequence 1, Application US/09790988

Patent No. 6632935

GENERAL INFORMATION:

APPLICANT: SHIGENOBU, SHUJI

APPLICANT: WATANABE, HIDEKI

APPLICANT: HATTORI, MASAHIRA

APPLICANT: SAKAKI, YOSHIYUKI

TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS

FILE REFERENCE: 081356/0159

CURRENT APPLICATION NUMBER: US/09/790,988

CURRENT FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: JP2000-107160

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 1

LENGTH: 640681

TYPE: DNA

ORGANISM: Buchnera sp.

US-09-790-988-1

Query Match 3.2%; Score 46.6; DB 4; Length 640681;

Best Local Similarity 46.3%; Pred. No. 0.094;

Matches 183; Conservative 0; Mismatches 211; Indels 1; Gaps 1;

QY 1 ATTATGATCTCAATACATACATATCTCATCTAGATCTAGATTATCATTTATGTAAG 60

DB 383471 ATAAAGGTAAGAAAGTTATTTAAAGAAATATATTTAAAGAAATGGTACTTGAAGAAAG 383530

QY 61 AAAGTTTTCAGCAATATGNNACGACAAATGGCTACACTCGATGTAATGGTATCTCAAC 120

DB 383531 TACCATTATTAATAATATATAATATTAATGATACACTGATTTAGGAGGTGTTTATA 383590

QY 121 TCACATTAATATACCAACATTAAGTAGGCAAAATTTAAACAACATATTTTATGATAT 180

DB 383591 AAAAATAAAATTTATTTTAAATATTTTATAGAGTAACGTAATTTTAAAAA 383650

QY 181 GCAAGAGTCAGCATATGATATGATTCAGATCGTTTTCAGCAGTTCGAGTAGTAG 240

DB 383651 TTTATTTTATATATTTTAAATAAAAAAATATATTTAAATAAAAAATTAAGTAAGTAT 383710

	Query Match	3.2%	Score 46.2	DB 2	Length 2448	
	Best Local Similarity	45.6%	Pred. No. 0.011			
	Matches 159	Conservative 0	Mismatches 190	Indels 0	Gaps 0	
Qy	73	AATATGNNACGACAAATGGCTACATCCGATCTAAATGGTATCTCAACTCAACATTATAC	132			
Db	2209	AATATACCTCTGTGAATTTGTTTAAACATGCTATTTCTACATCAATAGTTGAATTACAA	2150			
Qy	133	TTATACCAACCATTAGTTAGCAAAATTTAAACACATATTTTATGTATGCAAGATCAGC	192			
Db	2149	ATACTACAAGGTTTATTAATAATTAGCTTTAGCTGTAGTAATATATATTTAATTTGAATCG	2090			
Qy	193	ATATGTATTAATGATTCAGATCGCTTTTGACAGATTGGATGTAGTAGTACCATTTATTT	252			
Db	2089	ATATATTTCAAAAGGATCAGGTACTTTAGCTTCTGATATATATAATAATATACATGATT	2030			

Db	2089	ATATATTCAAAGAGTCAGTTTACTTTAGCTTCGATATATATATAAAATATACATGATTT	2030
QY	253	AATGTCATACTAATCGTGAATAGTGATATGATGAACAACTGTATCTATTGTGTAAATA	312
Db	2029	TCGAATTTTTTGATATATACAAAGATATTTCTTCGAAAATTCGGCAATTAATTTATCATTT	1970
QY	313	TCCATAAACACATCATGAAGACACATTTCTTTCAGGCTCGAATTAATTAATGATACAATT	372
Db	1969	TCAATAATATTTAAATATATAACCAAAATTTTTTAATAGTTTTTACTATTGTTTTTAATCTA	1910
QY	373	CTAATAGAAAACGAATTAATATACGTTGAATTGTATGAATCTAATTTGA	421
Db	1909	TATTTTACTACTAAAGTTTAATACACATCAATGAATATAATAATACCTAATAGA	1861

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RESULT 15
US-03-031-897-2/c
; Sequence 2, Application US/09031897
; Patent No. 6027895
; GENERAL INFORMATION:
; APPLICANT: Lambowitz, Alan
; APPLICANT: Mohr, Georg
; APPLICANT: Zimmerly, Steven
; APPLICANT: Gao, Huatuo
; TITLE OF INVENTION: Methods Cleaving DNA with Nucleoside
; TITLE OF INVENTION: Integrase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter & Griswold
; STREET: 800 Superior Avenue, Suite 1400
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: US
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031.897
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Docherty, Pamela A.
; REGISTRATION NUMBER: 40,591
; REFERENCE/DOCKET NUMBER: 24671/00105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216)622-8416
; TELEFAX: (216)241 0816
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2448 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
US-09-031-897-2

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Query Match	3.2%;	Score 46.2;	DB 3;	Length 2448;
Best Local Similarity	45.6%;	Pred. No. 0.011;		
Matches 159;	Conservative	0;	Mismatches 190;	Indels 0;
Gaps	0;			

QY	73	AATATGNNACGACAAATGGCTACACTCGAGTGAATTGSTATCTCAACTCAACATTATPAC	132
Db	2209	AATATACCTCTATGTAATTTGTTTAAACATGATGTATTTTACATCATCAATAGTTGAATTACAA	2150
QY	133	TTATACAAACAATTAGTTAGCAAAATTTAAACAATTTTTATGTATGCAAGAGTCAGC	192
Db	2149	ATACTACAAAGGTTTATTAAATTTAGCTTTAGCTGTAGTGAATATATATATTTAATTTGAATCG	2090
QY	193	ATATGTATTAATTCAGTTCGAATCGTTTTGACGAGTTCGAGTGTAGTAGTGCACATTATTT	252

QY 224 GAGTTCGGATGTAGTAGCCATTATTTAATGTGACATCTAATCTGTGAATGATGATG 283
Db |||||
QY 61 GAGTTCGGATGTAGTAGCCATTATTTAATGTGACATCTAATCTGTGAATGATGATG 120
Db |||||
QY 284 ATGAAACATTTGATCTTATTTCTAATAATATCCATAAACAACATCATGAAAGACATTTCTT 343
Db |||||
QY 121 ATGAAACATTTGATCTTATTTCTAATAATATCCATAAACAACATCATGAAAGACATTTCTT 180
Db |||||
QY 344 TCAGGGTCTGAATTAATTTATGATACATCTAATTAAGAAAAGAAATTAATTAACCTTGAAT 403
Db |||||
QY 181 TCAGGGTCTGAATTAATTTATGATACATCTAATTAAGAAAAGAAATTAATTAACCTTGAAT 240
Db |||||
QY 404 TGATGAAATCTAATTTGAACAGCCACACGACGAGCACTAAGCTTGCCTGGATGACT 463
Db |||||
QY 241 TGATGAAATCTAATTTGAACAGCCACACGACGAGCACTAAGCTTGCCTGGATGACT 300
Db |||||
QY 464 CGGTTTAAGTTAACTAAACAAAACGAGCTGTCTATGTAACACGCGGATCGACAGGTC 523
Db |||||
QY 301 CGGTTTAAGTTAACTAAACAAAACGAGCTGTCTATGTAACACGCGGATCGACAGGTC 360
Db |||||
QY 524 ACAGTCATGAAGCCATCAACGAAAGAACTAATCCAGGGGTGAGATGATTAATGTT 583
Db |||||
QY 361 ACAGTCATGAAGCCATCAACGAAAGAACTAATCCAGGGGTGAGATGATTAATGTT 420
Db |||||
QY 584 TAAATAATTTAGTTAAACACGAGGAAAA-GCTGTCTGACAGCCAGGTCACGTTATCTTTACC 642
Db |||||
QY 421 TAAATAATTTAGTTAAACACGAGGAAAAAGGCTGTCTGACAGCCAGGTCACGTTATCTTTACC 480
Db |||||
QY 643 TGTGGTCAAAATGATTCGTGTCTGCAATTTTAAATTTATTTTGAAGGCGGAAATAA 702
Db |||||
QY 481 TGTGGTCAAAATGATTCGTGTCTGCAATTTTAAATTTATTTTGAAGGCGGAAATAA 540
Db |||||
QY 703 AGTTGTAAGAGATAAACCAGGCTATATAAATTCATATATTTTCTCCCGCTTTGAATG 762
Db |||||
QY 541 AGTTGTAAGAGATAAACCAGGCTATATAAATTCATATATTTTCTCCCGCTTTGAATG 600
Db |||||
QY 763 TCTCGTGTCTCTCTCACTTTCATCAGCGGTTTGAATCTCCGCGACTTGACAGAGAAG 822
Db |||||
QY 601 TCTCGTGTCTCTCTCACTTTCATCAGCGGTTTGAATCTCCGCGACTTGACAGAGAAG 660
Db |||||
QY 823 AACAGGAAGAAGACTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTTCCGTTT 882
Db |||||
QY 661 AACAGGAAGAAGACTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTTCCGTTT 720
Db |||||
QY 883 TGAATCTCTCAATCTCACTTCTCTCCGCTCTTCTTCCAGGTAATGAGACTT 942
Db |||||
QY 721 TGAATCTCTCAATCTCACTTCTCTCCGCTCTTCTTCCAGGTAATGAGACTT 777
Db |||||
QY 943 TCTGGATCTACTTTATTTGTGCTGATCTCGATCTTCTTCTCAATTTCTTGGATCTGG 1002
Db |||||
QY 778 TCTGGATCTACTTTATTTGTGCTGATCTCGATCTTCTTCTCAATTTCTTGGATCTGG 837
Db |||||
QY 1003 AATTCGTTTAAATTTGATCTGTGAACTCCACTAAATCTTTTGGTTTCTAGAAATCGAT 1062
Db |||||
QY 838 AATTCGTTTAAATTTGATCTGTGAACTCCACTAAATCTTTTGGTTTCTAGAAATCGAT 897
Db |||||
QY 1063 CTAAGTTGACCGATCAGTTAGCTGATATAGTACAGAAATTTGGTTTCTAGAAATCGAT 1122
Db |||||
QY 898 CTAAGTTGACCGATCAGTTAGCTGATATAGTACAGAAATTTGGTTTCTAGAAATCGAT 957
Db |||||
QY 1123 AGAGATCCATTTGATTTAGCTGGAATGATTTGTATGTGAATTTGAATCTGAACT 1182
Db |||||
QY 958 AGAGATCCATTTGATTTAGCTGGAATGATTTGTATGTGAATTTGAATCTGAACT 1017
Db |||||
QY 1183 GTTGAAGTTAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1242
Db |||||
QY 1018 GTTGAAGTTAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1077
Db |||||
QY 1243 GTTGAAGTTAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1302
Db |||||
QY 1078 GTTGAAGTTAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1137
Db |||||
QY 1303 AACAGAAAGCTATTCTGATTCATTCAGGGTTTATTTGACTGTATTTGAATCTTTTGTG 1362
Db |||||

Db 1138 AACAGAAAGCTATTCTGATTCATTCAGGGTTTATTTGACTGTATGAACTCTTTTGTG 1197
QY 1363 TGTTTGCAGCTCATAAAAA 1382
Db 1198 TGTTTGCAGCTCATAAAAA 1217
RESULT 2
US-09-737-626A-9
; Sequence 9. Application US/09737626A
; Patent No. US20020144304A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flaisinski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. US20020144304A1el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/09/737,626A
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 9
; LENGTH: 1219
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1) .. (1219)
; OTHER INFORMATION: Act2 promoter: polynucleotide sequence and intron
US-09-737-626A-9
Query Match 81.4%; Score 1174.8; DB 9; Length 1219;
Best Local Similarity 98.7%; Pred. No. 4.6e-270;
Matches 1206; Conservative 0; Mismatches 12; Indels 4; Gaps 2;
QY 164 GAACATATTTTATGTATGACAGAGTGTGATATGATTAATGATTCAGAAATCGTTTGAC 223
Db 1 CAACATATTTTATGTATGACAGAGTGTGATATGATTAATGATTCAGAAATCGTTTGAC 60
QY 224 GAGTTCGGATGTAGTAGCCATTATTTAATGTGACATCTAATCTGTGAATGATGATG 283
Db 61 GAGTTCGGATGTAGTAGCCATTATTTAATGTGACATCTAATCTGTGAATGATGATG 120
QY 284 ATGAAACATTTGATCTTATTTCTAATAATATCCATAAACAACATCATGAAAGACATTTCTT 343
Db 121 ATGAAACATTTGATCTTATTTCTAATAATATCCATAAACAACATCATGAAAGACATTTCTT 180
QY 344 TCAGGGTCTGAATTAATTTATGATACATCTAATTAAGAAAAGAAATTAATTAACCTTGAAT 403
Db 181 TCAGGGTCTGAATTAATTTATGATACATCTAATTAAGAAAAGAAATTAATTAACCTTGAAT 240
QY 404 TGATGAAATCTAATTTGAACAGCCACACGACGAGCACTAAGCTTGCCTGGATGACT 463
Db 241 TGATGAAATCTAATTTGAACAGCCACACGACGAGCACTAAGCTTGCCTGGATGACT 300
QY 464 CGGTTTAAGTTAACTAAACAAAACGAGCTGTCTATGTAACACGCGGATCGACAGGTC 523
Db 301 CGGTTTAAGTTAACTAAACAAAACGAGCTGTCTATGTAACACGCGGATCGACAGGTC 360
QY 524 ACAGTCATGAAGCCATCAACGAAAGAACTAATCCAGGGGTGAGATGATTAATGTT 583
Db 361 ACAGTCATGAAGCCATCAACGAAAGAACTAATCCAGGGGTGAGATGATTAATGTT 420
QY 584 TAAATAATTTAGTTAAACACGAGGAAAA-GCTGTCTGACAGCCAGGTCACGTTATCTTTACC 642
Db 421 TAAATAATTTAGTTAAACACGAGGAAAAAGGCTGTCTGACAGCCAGGTCACGTTATCTTTACC 480
QY 643 TGTGGTCAAAATGATTCGTGTCTGCAATTTTAAATTTATTTTGAAGGCGGAAATAA 702
Db 481 TGTGGTCAAAATGATTCGTGTCTGCAATTTTAAATTTATTTTGAAGGCGGAAATAA 540
Db |||||


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; TITLE OF INVENTION: No. US20020144304A1el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/09/737,626A
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 1742
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1742)
; OTHER INFORMATION: chimeric promoter fusion CamV and Act2 polynucleotides + Act2 in
; OTHER INFORMATION: tto
US-09-737-626A-30

Query Match      81.3%; Score 1174; DB 9; Length 1742;
Best Local Similarity 99.3%; Pred. No. 8.5e-270;
Matches 1201; Conservative 0; Mismatches 5; Indels 4; Gaps 2;

QY 164 CAACATATTTTATGATGCAAGAGTCAGCATATGATTAATGATTCAGAAATCGTTTTCAC 223
DB 533 CAACATATTTTATGATGCAAGAGTCAGCATATGATTAATGATTCAGAAATCGTTTTCAC 592
QY 224 GAGTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 283
DB 593 GAGTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 652
QY 284 ATGAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 343
DB 653 ATGAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 712
QY 344 TCAGGGTCTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 403
DB 713 TCAGGGTCTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 772
QY 404 TGTATGAATCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 463
DB 773 TGTATGAATCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 832
QY 464 CGGTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 523
DB 833 CGGTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 892
QY 524 ACAGTCATGAAGCCATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 583
DB 893 ACAGTCATGAAGCCATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 952
QY 584 TAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 642
DB 953 TAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1012
QY 643 TGTGTCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 702
DB 1013 TGTGTCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1072
QY 703 AGTTGTAAGAGATAAACCCGCTATATAAATTCATATATTTTCTCCCGCTTTTGAATG 762
DB 1073 AGTTGTAAGAGATAAACCCGCTATATAAATTCATATATTTTCTCCCGCTTTTGAATG 1132
QY 763 TCTCGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 822
DB 1133 TCTCGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1192
QY 823 AACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 882
DB 1193 AACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1252
QY 883 TGAATCTTCTCAATCTCAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 942
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DB 1253 TGAATCTTCTCAATCTCAATCTCAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1309
QY 943 TCTGGATCTACTTTTATTTCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGGAT 1002
DB 1310 TCTGGATCTACTTTTATTTCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGG 1369
QY 1003 AATTGGTTTAAATTTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGG 1062
DB 1370 AATTGGTTTAAATTTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGG 1429
QY 1063 CTAAGTTGACCGATCAGTTAGCTCGATTTATAGTACAGAAATTTGGCTTGAACCTTGGTGG 1122
DB 1430 CTAAGTTGACCGATCAGTTAGCTCGATTTATAGTACAGAAATTTGGCTTGAACCTTGG 1499
QY 1123 AGAGATCCATGTTTACCTGGGAAATGATTTGATATGATGATGATGATGATGATGATGATG 1182
DB 1490 AGAGATCCATGTTTACCTGGGAAATGATTTGATATGATGATGATGATGATGATGATGAT 1549
QY 1183 GTTGAAGTTAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1242
DB 1550 GTTGAAGTTAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1609
QY 1243 GTTGAAGTTAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1302
DB 1610 GTTGAAGTTAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1669
QY 1303 AACAGAAAGCTATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1362
DB 1670 AACAGAAAGCTATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1729
QY 1363 TGTGTCGAGC 1372
DB 1730 TGTGTCGAGC 1739

RESULT 6
US-10-427-169-30
; Sequence 30, Application US/10427169
; Publication No. US20030199681A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flaszinski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. US20030199681A1el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/427,169
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: US/09/737,626A
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 1742
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1742)
; OTHER INFORMATION: chimeric promoter fusion CamV and Act2 polynucleotides + Act2 in
; OTHER INFORMATION: tto
US-10-427-169-30

Query Match      81.3%; Score 1174; DB 14; Length 1742;
Best Local Similarity 99.3%; Pred. No. 8.5e-270;
Matches 1201; Conservative 0; Mismatches 5; Indels 4; Gaps 2;

QY 164 CAACATATTTTATGATGCAAGAGTCAGCATATGATTAATGATTCAGAAATCGTTTTCAC 223
DB 533 CAACATATTTTATGATGCAAGAGTCAGCATATGATTAATGATTCAGAAATCGTTTTCAC 592
QY 224 GAGTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 283
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Db	1670	ACAGAAAGCTATTTCTGATTCAGGGTTATTTGACTGATGAATCACTCTTTTGG	1729
Qy	1363	TGTTGCAGC	1372
Db	1730	TGTTGCAGC	1739
RESULT 7			
US-10-427-180-30			
; Sequence 30, Application US/10427180			
; Publication No. US20030199682A1			
; GENERAL INFORMATION:			
; APPLICANT: Fincher, Karen			
; APPLICANT: Plasinski, Stanislaw			
; APPLICANT: Wilkinson, Jack			
; TITLE OF INVENTION: No. US20030199682A1e1 Plant Expression Constructs			
; FILE REFERENCE: 38-21(51:499)B			
; CURRENT APPLICATION NUMBER: US/10/427,180			
; CURRENT FILING DATE: 2003-05-01			
; PRIOR APPLICATION NUMBER: US/09/737,626A			
; PRIOR FILING DATE: 2002-02-25			
; PRIOR APPLICATION NUMBER: 09/737,626			
; PRIOR FILING DATE: 2000-12-15			
; NUMBER OF SEQ ID NOS: 30			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 30			
; LENGTH: 1742			
; TYPE: DNA			
; ORGANISM: artificial sequence			
; FEATURE:			
; NAME/KEY: promoter			
; LOCATION: (1)..(1742)			
; OTHER INFORMATION: chimeric promoter fusion CamV and Act2 polynucleotides +			
; OTHER INFORMATION: tro			
US-10-427-180-30			
Query Match 81.3%; Score 1174; DB 14; Length 1742;			
Best Local Similarity 99.3%; Pred. No. 8.5e-270;			
Matches 1201; Conservative 0; Mismatches 5; Indels 4; Gaps 2;			
Qy	164	CAACTATTTTGTATGTCAGAGCTCAGCATATGTATATTTGATTTCAGATTCGTTTTCAC	223
Db	533	CAACTATTTTGTATGTCAGAGCTCAGCATATGTATATTTGATTTCAGATTCGTTTTCAC	592
Qy	224	GAGTTCGAGTGTAGTAGTACCAATTTTAAATGTACATCTAATCGTGAATGTGATATG	283
Db	593	GAGTTCGAGTGTAGTAGTACCAATTTTAAATGTACATCTAATCGTGAATGTGATATG	652
Qy	284	ATGAAACATGTATCTTATCTGTAATATATCCATAACACATCATCAAGAAGACACTTTCT	343
Db	653	ATGAAACATGTATCTTATCTGTAATATATCCATAACACATCATCAAGAAGACACTTTCT	712
Qy	344	TCAGGCTCGAATTAATATATGATACAATTTCTAATAGAAAACGAATTAATTTACGTTGAAT	403
Db	713	TCAGGCTCGAATTAATATATGATACAATTTCTAATAGAAAACGAATTAATTTACGTTGAAT	772
Qy	404	TGTAAGAAATCTAATTTGAACAGGCAACACACGACGAGCTAACGTTGCCTGGATTGACT	463
Db	773	TGTAAGAAATCTAATTTGAACAGGCAACACGACGAGCTAACGTTGCCTGGATTGACT	832
Qy	464	CGGTTTAAGTTTAACCACTAAAAAAAACGAGCTGTCTATGTAACACGCGGATCGACGAGTTC	523
Db	833	CGGTTTAAGTTTAACCACTAAAAAAAACGAGCTGTCTATGTAACACGCGGATCGACGAGTTC	892
Qy	524	ACAGTCATGAAGCCATCAAGCAAGAAAGACTAATCCAAAGGGGTGAGATGATTAATTAGTT	583
Db	893	ACAGTCATGAAGCCATCAAGCAAGAAAGACTAATCCAAAGGGGTGAGATGATTAATTAGTT	952
Qy	584	TAAAAATTAGTTTAACACGAGGGAAA- -GCTGCTGTACACGACGAGTTCAGTTATCTTTACC	642
Db	953	TAAAAATTAGTTTAACACGAGGGAAAAGGCTGTGTGACGACGAGTTCAGTTATCTTTACC	1012
Qy	643	TGTGGTCGAAATGATTCGTGTCTCTCGATTTTAATTTATTTTTTTTGAAGGCCGAAATAA	702

Db 1013 TGTGTCGAATGATTCGTGCTGCGATTTTAAATTAATTTTGTGAAGCCGAAATPAA 1072
QY 703 AGTCTAAGAGATAAACCCGCTATATATAATTTTCCCTCCCGCTTTGAATTTG 762
Db 1073 AGTCTAAGAGATAAACCCGCTATATATAATTTTCCCTCCCGCTTTGAATTTG 1132
QY 763 TCTCGTTGCTCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 822
Db 1133 TCTCGTTGCTCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 1192
QY 823 AACAGGAG 882
Db 1193 AACAGGAG 1252
QY 883 TGAATCTCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAAT 942
Db 1253 TGAATCTCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAAT 1309
QY 943 TCTGGATCTACTTTATTTGCTCGATCTCGATCTCGATCTCGATCTCGATCTCGAT 1002
Db 1310 TCTGGATCTACTTTATTTGCTCGATCTCGATCTCGATCTCGATCTCGATCTCGAT 1369
QY 1003 AATTCGTTTAAATTTGAGATCTGTGAACCTCCCACTAAATCTTTTGGTTTACTAGATCGAT 1062
Db 1370 AATTCGTTTAAATTTGAGATCTGTGAACCTCCCACTAAATCTTTTGGTTTACTAGATCGAT 1429
QY 1063 CTAAAGTGAAGATCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAG 1122
Db 1430 CTAAAGTGAAGATCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAG 1489
QY 1123 AGAGATCCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1182
Db 1490 AGAGATCCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1549
QY 1183 GTTGAAGTGAAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1242
Db 1550 GTTGAAGTGAAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1609
QY 1243 GTTAGATGAAGTGTGTAGATCTGTGAACCTTCCGAACTTTAGATTTGTAGTGTGTAGTGTG 1302
Db 1610 GTTAGATGAAGTGTGTAGATCTGTGAACCTTCCGAACTTTAGATTTGTAGTGTGTAGTGTG 1669
QY 1303 AACAGAAAGCTATTTCTGATCTCAATCAGGCTTTATTTGATCTGATCTGATCTGATCTGAT 1362
Db 1670 AACAGAAAGCTATTTCTGATCTCAATCAGGCTTTATTTGATCTGATCTGATCTGATCTGAT 1729
QY 1363 TGTTCGAGC 1372
Db 1730 TGTTCGAGC 1739

RESULT 8
US-09-887-384A-5
; Sequence 5, Application US/09887384A
; Patent No. US2002049992A1
; GENERAL INFORMATION:
; APPLICANT: Hamilton, Carol
; TITLE OF INVENTION: MODIFIED PROMOTERS
; FILE REFERENCE: actin promoters
; CURRENT APPLICATION NUMBER: US/09/887,384A
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1259
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Actin based
; OTHER INFORMATION: promoter
US-09-887-384A-5

Query Match 76.58; Score 1104.6; DB 9; Length 1259;
Best Local Similarity 94.08; Pred. No. 2.7e-253;
Matches 1198; Conservative 0; Mismatches 59; Indels 18; Gaps 4;
QY 164 CAACATATTTTATGATGCAAGAGTCAGCATATGTAATTAATTCAGATTCGTTTGTAC 223
Db 1 CAACATATTTTATGATGCAAGAGTTTCATCTTGATATTAATTCAGATTCGTTTGTAC 60
QY 224 GAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 283
Db 61 GAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
QY 284 ATCAACATCTGATCTTATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 343
Db 121 ATCAACATCTGATCTTATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
QY 344 TCAGGTCCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 403
Db 181 TCAGGTCCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
QY 404 TGATGAAATCTAATTTGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 463
Db 241 TGATGAAATCTAATTTGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 300
QY 464 CGGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 523
Db 301 AAGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
QY 524 ACAGTCATGAAGCCATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 583
Db 361 ACAGTCATGAAGCCATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 420
QY 584 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 642
Db 421 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
QY 643 TGTGTCGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 702
Db 481 TGTGTCGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
QY 703 AGTTTGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 762
Db 541 AGTTTGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
QY 763 TCTGTCGTCCT 822
Db 601 TCTGTCGTCCT 660
QY 823 AACAGGAG 882
Db 661 AACAGGAG 706
QY 883 TGAATCTCTCAATCTCAATCTCTCAATCTCTCAATCTCTCAATCTCTCAATCTCTCAATCTCT 942
Db 707 TGAATCTCTCAATCTCTCAATCTCTCAATCTCTCAATCTCTCAATCTCTCAATCTCTCAATCTCT 763
QY 943 TCTGGATCTACTTTATTTGCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGG 1002
Db 764 TCTGGATCTACTTTATTTGCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGGATCTGG 823
QY 1003 AATTCGTTTAAATTTGAGATCTGTGAACCTCCCACTAAATCTTTTGGTTTACTAGATCGAT 1062
Db 824 TTTTCGTTTAAATTTGAGATCTGTGAACCTCCCACTAAATCTTTTGGTTTACTAGATCGAT 883
QY 1063 CTAAAGTGAAGATCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAG 1122
Db 884 CTAAAGTGAAGATCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAG 943
QY 1123 AGAGATCCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1182
Db 944 AGAGATCCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1003
QY 1183 GTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1242

Query Match	72.9%	Score 1053	DB 9	Length 1202	
Best Local Similarity	94.0%	Pred. No. 5.4e-241			
Matches 1144	Conservative	0	Mismatches 55	Indels 18	Gaps 4
QY	164	CAACATATTTTGTATGTAACGAGGTGAGCATATGTATAATTGATTCAGAAATCGTTTGGAC	223		
DB	1	CAACTATTTTGTATGTAACGAGGTTCATCTGTATTAATTGATTCAGAAATCGTTTGGAC	60		
QY	224	GAGTTCGGATGTAGTAGTAGGCATATTTTAATGTACATATTAATCGTGAATPAGTATAG	283		
DB	61	GAGTTCCGATGTAGTAGTAGGCATATTTTAATGTACATATTAATCGTGAATPAGTATAG	120		
QY	284	ATGAACAATCTGATCTTATTGTATATAATATCCATAACACATCATCGAAGAACAATTTCTT	343		
DB	121	ATGAACAATCTGATCTTATTGTATATAATATCCATAACACATCATCGAAGAACAATTTCTT	180		
QY	344	TCAGGTCGTGAATTAATATGATACAAATCTTAATAGAAAAAGAAATTAATACGTTTGAAT	403		
DB	181	TCAGGTCGTGAATTAATATGATACAAATCTTAATAGAAAAAGAAATTAATACGTTTGAAT	240		
QY	404	TGTTGTGAATCTTAATTTGACACAGCCACACGACGAGGACTACGTTTGCCTGGATTGACT	463		
DB	241	TGTTGTGAATCTTAATTTGACACAGCCACACGACGAGGACTTAACGTTTGCCTGGAAATGAA	300		
QY	464	CGGTTTAAAGTTAAACCACTAAAAAACCGAGCTGTCATGTAAACACGCGGATCGAGCAGGTC	523		
DB	301	AAGTTTAAAGTAACCACTAAAAAACCGAGCTGTCATGTAAACACGCGGATCGAGCAGGTC	360		
QY	524	ACAGTCATGAAGCCATCAAGCCAAAGACATTAATCCGAGGGGTGAGATGATTAAATTTAGTT	583		
DB	361	ACAGTCATGAAGCCATCAAGCCAAAGACATTAATCCGAGGGGTGAGATGATTAAATTTAGTT	420		

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RESULT 10
US-09-887-384A-6
; Sequence 6, Application US/09887384A
; Patent No. US20020049592A1
;
GENERAL INFORMATION:
; APPLICANT: Hamilton, Carol
; TITLE OF INVENTION: MODIFIED PROMOTERS
; FILE REFERENCE: actin promoters
; CURRENT APPLICATION NUMBER: US/09/887,384A
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1342
; TYPE: DNA
; ORGANISM: Artificial Sequence
;

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QY 451 GCCTGATTCACCTCGTTTAACTTAACCACTAAATAAAGCGAGCTGTCTATGACAGCG 510
Db 312 GCCTGGAATGAAGAAAGTTTAAAGTAACCACTAAATAAAGCGAGCTGTCTATGACAGCG 371
QY 511 GATCGAGAGGTCAAGT-----CATGAAGCCATCAAGCAAAAGAACTAATCCAGGGG 565
Db 372 GATCGAGAGGTCAAGTCAATCCATGAAGCCATCAAGCAAAAGAACTAATCCAGGGG 431
QY 566 TGAGATGATTAATTAAGTTTAAATTAAGTTTAACTTAACCAAGGGAAGAA--GCTGTCTGACAGCA 624
Db 432 TGAGATGATTAATTAAGTTTAAATTAAGTTTAACTTAACCAAGGGAAGGCTGTCTGACAGCA 491
QY 625 GGTCAAGTTA---TCTTTACCTGTGTCGAATGATTCGTCTGTCGATTTTAAATTAAT 681
Db 492 GGTCAAGTTAATCTTCTTACCTGTGTCGAATGATTCGTCTGTCGATTTTAAATTAAT 551
QY 682 T-----TTTTGAAGCCGCAAAATAAAGTTGTAAGATTAACCCGCTCATATAA 731
Db 552 TCCAAATTAATTTGAAGCCGCAAAATAAAGTTGTAAGATTAACCCGCTCATATAA 611
QY 732 ATTCAAT-----ATATTTCTCTCCGCTTTTGAATTCGTCTGTCGCTCTCTCACT 782
Db 612 ATTCAATCAACCTCGATATTTCTCTCCGCTTTTGAATTCGTCTGTCGCTCTCTCACT 671
QY 783 TCATCAGCGCTTTTGAATCTCCGCGACTTGACAGAGAAACAGAGGAAGAACTAAGA 842
Db 672 TCATCAGCGCTTTTGAATCTCCGCGACTTGACAGAGAAACAGAGGAAGAACTAAGA 731
QY 843 GAGAAATGAAGATTAATCAAGAGATTCATTCGCTGTTTGAATTCCTCAATCTCAT 902
Db 732 GAGAAATGAAGATTAATCAAGAGATTCATTCGCTGTTTGAATTCCTCAATCTCAT 790
QY 903 CTTCTCTCCGCTTTTCTTCCAGGTAATAGCACTTC--TGGATCTATTTATTTG 961
Db 791 --TCTTCTCCGCTTTTCTTCCAGGTAATAGCACTTC--TGGATCTATTTATTTG 848
QY 962 CTGATCTCGATCTTGTCTTCTCAATTTCTTGATGATCTGGAATTCG--TTTAAATTTGA 1019
Db 849 CTGATCTCGATCTTGTCTTCTCAATTTCTTGATGATCTGGAATTCG--TTTAAATTTGA 908
QY 1020 TCTGTGAACCTCACTAAATCTTTTGTGTTTACTAGATCGATCAAGTTCACCGATCAG 1079
Db 909 TCGAATTTAGATCACTAAATCTTTTGTGTTTACTAGATCGATCAAGTTCACCGATCAG 968
QY 1080 TTAGCTGATTAAGTACAGAAATTTGGCTTGACCTTGATGAGAA--GATCCATCTTC 1136
Db 969 TTAGCTGATTAAGTACAGAAATTTGGCTTGACCTTGATGAGAA--GATCCATCTTC 1028
QY 1137 ATGTTACCTGGGAAATGATTTGTATATGTGAATTTGAATCTGA--ACTGTTGAAGTTAGA 1194
Db 1029 ATGTTACCTGGGAAATGATTTGTATATGTGAATTTGAATCTGA--ACTGTTGAAGTTAGA 1088
QY 1195 TTGAATCTGAACACTCAATGTTTGAATTTGAATCTGAACACTGTTTAAAGTTAGATGAAGT 1254
Db 1089 TTATGATCTGAACACTCAATGTTTGAATTTGAATCTGAACACTGTTTAAAGTTAGATGAAGT 1148
QY 1255 TTGTGTATAGATTTCTGAAACCTTAGGATTTGTAGTCTGATGTTGAACAGAAAGCTA 1314
Db 1149 TTGTGTATAGATTTCTGAAACCTTAGGATTTGTAGTCTGATGTTGAACAGAAAGCTA 1208
QY 1315 TTCTGATTAATCAATCAGGGT-----TATTTGATGATTAAGTCAATCTTTTGTGTTG 1364
Db 1209 TTCTGATTAATCAATCAGGGT-----TATTTGATGATTAAGTCAATCTTTTGTGTTG 1268
QY 1365 TTTCAGCTCATAAA 1379
Db 1269 TTTCAGCTCATAAA 1283

RESULT 12
US-09-867-384A-4
; Sequence 4, Application US/09887384A

; Patent No. US2002004992A1
; GENERAL INFORMATION:
; APPLICANT: Hamilton, Carol
; TITLE OF INVENTION: MODIFIED PROMOTERS
; FILE REFERENCE: actin promoters
; CURRENT APPLICATION NUMBER: US/09/887,384A
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4
; LENGTH: 910
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Actin based
; OTHER INFORMATION: promoter
US-09-887-384A-4

Query Match 54.3%; Score 784.4; DB 9; Length 910;
Best Local Similarity 93.6%; Pred. No. 6.1e-177;
Matches 867; Conservative 0; Mismatches 41; Indels 18; Gaps 4;
QY 513 TCGAGCAGGTCAAGTCAATGAAGCCATCAAGCAAAAGAACTAATCCAGGGGTGAGATG 572
Db 1 TCGAGCAGGTCAAGTCAATGAAGCCATCAAGCAAAAGAACTAATCCAGGGGTGAGATG 60
QY 573 ATTAATTAAGTTTAAATAATTAAGTTTAAACAGGAGGAAA--GCTGTCTGACAGCCAGTCAAG 631
Db 61 ATTAATTAAGTTTAAATAATTAAGTTTAAACAGGAGGAAAGGCTGTCTGACAGCCAGTCAAG 120
QY 632 TTATCTTTACTGTGTGTCGAAATGATTCGTGTCTGTCTGATTTTAAATTTTGTGAAAG 691
Db 121 TTATCTTTACTGTGTGTCGAAATGATTCGTGTCTGTCTGATTTTAAATTTTGTGAAAG 180
QY 692 GCGCAATAAAGTGTGAAGAGATAACCGCGCTATATAAATTCATATTTTCTCTCCC 751
Db 181 GCGCAATAAAGTGTGAAGAGATAACCGCGCTATATAAATTCATATTTTCTCTCCC 240
QY 752 GCTTTGAATTTGTCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 811
Db 241 GCTTTGAATTTGTCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 812 TCACAGAGAAAGCAAGGAAAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTC 871
Db 301 TCACAGAGAAAGCAAGGAAAG--AGAGAGAAAGTAAGAGATAATCCAGG-- 347
QY 872 ATTCCTCGTTTGAATTTCTCTCAATCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCAAGGT 931
Db 348 -TTCTCCGTTTGAATCAAGGT 403
QY 932 AATAGGAACCTTCTGGATCTACTTTATTTGCTGGATCTCGATCTCTGTTTCTCAATTTCC 991
Db 404 AATAGGAACCTTCTGGATCTACTTTATTTGCTGGATCTCGATCTCTGTTTCTCAATTTCC 463
QY 992 TTGAGATCTGGAATTCGTTTAAATTTGGAATCTGGAACCTCCACTTAATCTTTTGGTTTAA 1051
Db 464 TTGAGATCTGGAATTCGTTTAAATTTGGAATCTGGAATTTAGATCACTAAATCTTTTGGTTTAA 523
QY 1052 CTAGAATCTGATCTAAGTGAAGCCGATCAGTTAGTCTGATTAAGTACCAGAAATTTGGCTT 1111
Db 524 CTAGAATCTGATCTAAGTGAAGCCGATCAGTTAGTCTGATTAAGTACCAGAAATTTGGCTT 583
QY 1112 GACCTTGATCGAGAGATCAATGTTTCAATGTTTACCTGGAAATGATTTGTATATGTAATG 1171
Db 584 GACCTTGATCGAGAGATCAATGTTTCAATGTTTACCTGGAAATGATTTGTATATGTAATG 643
QY 1172 AAACTGAACTGTTGAGTTAGATTTGAATCTGAACTGTAATCTGTAATCTAGATTAATCTGA 1231
Db 644 AAACTGAACTGTTGAGTTAGATTTGAATCTGTAATCTGTAATCTAGATTAATCTGA 703
QY 1232 ACACCTGTTTAAAGTTAGATGAAGTTTGTATAGATTTCTTCCAAACCTTAGGATTTGTAGT 1291
Db 704 TAACTGTTTAAAGTTAGATGAAGTTTGTATAGATTTCTTCCAAACCTTAGGATTTGTAGT 763

QY 1292 GTCGACGTTGACGAGAAAGCTATTCTGATTCATACGAGGTTTATTGACTGTATTGAA 1351
Db 764 GTCGACGTTGACGAGAAAGCTATTCTGATTCATACGAGGTTTATTGACTGTATTGAA 823
QY 1352 CTCCTTTTGTGTTTGGAGCTCATAAAAAAGGCTGAGGCTGACGATTAATCAACCAATC 1411
Db 824 CTCCTTTTGTGTTTGGAGCTCATAAAAAAGGCTGAGGCTGAGGCTGATTAATCAACCAATC 983
QY 1412 GTGTGTGCAATGGTACTGGAATGGT 1437
Db 884 GTGTGTGCAATGGTACTGGAATGGT 909

RESULT 13

US-09-887-384A-1

; Sequence 1, Application US/09887384A

; Patent No. US20020049992A1

; GENERAL INFORMATION:

; APPLICANT: Hamilton, Carol

; TITLE OF INVENTION: MODIFIED PROMOTERS

; FILE REFERENCE: actin promoters

; CURRENT APPLICATION NUMBER: US/09/887,384A

; CURRENT FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 853

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: promoter

US-09-887-384A-1

Query Match 50.7%; Score 732.8; DB 9; Length 853;
Best Local Similarity 93.7%; Pred. No. 1.2e-164;
Matches 813; Conservative 0; Mismatches 37; Indels 18; Gaps 4;

QY 513 TCGAGCAGGTCACGTCATGAGCCATCAAGCAAGAACTAATCCAGGGGTGAGATG 572
Db 1 TCGAGCAGGTCACGTCATGAGCCATCAAGCAAGAACTAATCCAGGGGTGAGATG 60
QY 573 ATTAATTAGTTTAAAAAATAGTTAAACACAGGGAAGA-GCTGTCTGACAGCCAGGTCAAG 631
Db 61 ATTAATTAGTTTAAAAAATAGTTAAACACAGGGAAGAAGCTGTCTGACAGCCAGGTCAAG 120
QY 632 TTATCTTTACCTGTGTGCGAAATGANTGCTGTCTGCAATTTAAATTTATTTTGTGAAG 691
Db 121 TTATCTTTACCTGTGTGCGAAATGANTGCTGTCTGCAATTTAAATTTATTTTGTGAAG 180
QY 692 GCCGAAATAAGTTGTAAGAGATAAACCGCTATATAATTCATATATTTCTCTCCC 751
Db 181 GCCGAAATAAGTTGTAAGAGATAAACCGCTATATAATTCATATATTTCTCTCCC 240
QY 752 GCTTTGAATTTGCTGCTGCTCTCCTCATCTTTTCATCAGCGTTTGAATCTCCGCGACT 811
Db 241 GCTTTGAATTTGCTGCTGCTCTCCTCATCTTTTCATCAGCGTTTGAATCTCCGCGACT 300
QY 812 TGACAGAGAGAACAGAGAGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTC 871
Db 301 TGACAGAGAGAACAGAGAGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTC 347
QY 872 ATTCTCGGTTTGAATCTTCGCAATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 931
Db 348 -TTCTCGGTTTGAATCTTCGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 403
QY 932 AATAGGAATCTTCTGGAATCTACTTTATTTTCTGGAATCTGATCTGTTTCTCTCAATTTCC 991
Db 404 AATAGGAATCTTCTGGAATCTACTTTATTTTCTGGAATCTGATCTGTTTCTCTCAATTTCC 463
QY 992 TTGAGATCTGGAATCTGTTTAAATTTGGATCTGTGAACCTCCATAATCTTTTGGTTTTTA 1051
Db 464 TTGAGATCTGTTTAAATTTTAAATTTGGATGGAATTTAGATCACTAAATCTTTTGGTTTTTA 523

QY 1052 CTAGATCGATCTAAGTTGACCGATCAGTTAGCTCGATTATAGCTACCAAGATTTGGCTT 1111
Db 524 CTAGATCGATCTAAGTTGACCGATCAGTTAGCTCGATTATAGCTACCAAGATTTGGCTT 583
QY 1112 GACCTTGATCGAGAGATCCATGTTTCATGTTTACCTGGGAAATGATTTGTATATGCTGAATG 1171
Db 584 GACCTTGATCGAGAGATCCATGTTTCATGTTTACCTGGGAAATGATTTGTATATGCTGAATG 643
QY 1172 AAATCTGAATCTGTTGAAGTTAGATTAGATCTGAAACACTGTCAATGTTAGATTGAATCTGA 1231
Db 644 AAATCTGAATCTGTTGAAGTTAGATTAGATTAGATCTGAAACACTGTCAATGTTAGATTGAATG 703
QY 1232 ACACCTGTTTAAAGTTAGATCAAGTTTGTGTATAGATTCTTCGAAACCTTAGGATTTGTAGT 1291
Db 704 TAACTGTTTAAAGTTAGATCAAGTTTGTGTATAGATTCTTCGAAACCTTAGGATTTGTAGT 763
QY 1292 GTCGTACGTTGAAACAGAAAGCTATTCTGATTCATCAATCAGGGTTTATTGACTGTATTGAA 1351
Db 764 GTCGTACGTTGAAACAGAAAGCTATTCTGATTCATCAATCAGGGTTTATTGACTGTATTGAA 823
QY 1352 CTCCTTTTGTGTTTGGAGCTCATAAA 1379
Db 824 CTCCTTTTGTGTTTGGAGCTCATAAA 851

RESULT 14

US-10-425-114-14693

; Sequence 14693, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 14693

; LENGTH: 1468

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; OTHER INFORMATION: Clone ID: L1B24-131-F9_FLI

US-10-425-114-14693

Query Match 10.0%; Score 144; DB 12; Length 1468;
Best Local Similarity 92.8%; Pred. No. 5.8e-24;
Matches 163; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

QY 776 CTCACCTTTTCATCAGCCGCTTTTGAATCTCCGCGACTTGACAGAGAGAACAGAGAGAG 835
Db 1 CTCACCTTTTCATCAGCCGCTTTTGAATCTCCGCGACTTGACAGAGAGAACAGAGAGAG 60
QY 836 ACTAAGAGAGAGAGTAAGAGATATCCAGAGATTCATCTCCGTTTGAATCTCTCTCA 895
Db 61 ACTAAGAGAGAGAGTAAGAGATATCCAGAGATTCATCTCCGTTTGAATCTCTCTCA 120
QY 896 ATCTCATCTCTCTCTCCGCTCTTTCTTTTCCAGGTAATAGAACTTTCTGGATCT 951
Db 121 ATCTCA---TCTCTCTCCGCTCTTTCTTTTCCAGCTCATAAAAAATGGCTGAGGT 173

RESULT 15

US-09-887-384A-14

; Sequence 14, Application US/09887384A

; Patent No. US20020049992A1

; GENERAL INFORMATION:

Mon Mar 15 10:37:55 2004

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; APPLICANT: Hamilton, Carol
; TITLE OF INVENTION: MODIFIED PROMOTERS
; FILE REFERENCE: actin promoters
; CURRENT APPLICATION NUMBER: US/09/887,384A
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA fragments
; OTHER INFORMATION: for assembling an actin-based promoter
US-09-887-384A-14

Query Match      6.5%; Score 94; DB 9; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1059 CGATCTAAGTTGACCGATCAGTACGCTCGATTATAGCTACCAAGATTGGCTTGACCTTG 1118
DB      1 CGATCTAAGTTGACCGATCAGTACGCTCGATTATAGCTACCAAGATTGGCTTGACCTTG 60

QY      1119 ATGGAGAGATCCATGTTTCATGTTACCTGGGAAT 1152
DB      61 ATGGAGAGATCCATGTTTCATGTTACCTGGGAAT 94
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Search completed: March 15, 2004, 05:20:22
Job time : 1422 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2004, 22:37:13 ; Search time 4056 Seconds

(without alignments)

10527.585 Million cell updates/sec

Title: US-09-868-744B-1

Perfect score: 1444

Sequence: 1 attatgatctcaataacatt.....gtactggaatggtagatccc 1444

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hcc:*

9: gb_estl:*

10: gb_est2:*

11: gb_hcc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_plg:*

27: em_gss_vrl:*

28: gb_gssl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
C 1	272.8	18.9	552	29	BX531590 Arabidops
2	202.4	14.0	327	9	AV831431
3	166	11.5	600	9	AV831862
4	163	11.3	546	9	AV525527

5	158	10.9	396	9	AV828177
6	158	10.9	562	9	AV830541
7	158	10.9	580	9	AV831261
8	158	10.9	667	9	AV824265
9	156	10.8	538	9	AV526249
10	153	10.6	399	9	AV829675
11	151	10.5	297	9	AV525898
12	150	10.4	162	28	BH901724
13	147	10.2	774	13	BU635286
14	146	10.1	463	14	N65062
15	144	10.0	438	14	N38049
16	144	10.0	597	14	T46735
17	143.8	10.0	382	9	AV545656
18	143	9.9	352	14	Z25952
19	143	9.9	393	14	T43759
20	142	9.8	411	14	R65270
21	139.4	9.7	253	14	T20889
22	138.4	9.6	897	14	CF652111
23	136	9.4	454	9	AV525074
24	136	9.4	512	9	AV525969
25	136	9.4	518	9	AV525842
26	132	9.1	370	14	T21821
27	132	9.1	446	14	CB253737
28	131	9.1	710	10	B8038458
29	131	9.1	915	14	CF652259
30	129.4	9.0	458	14	CB264030
31	126	8.7	540	9	AV550855
32	125	8.7	449	14	CF651398
33	124	8.6	412	14	R29797
34	123	8.5	426	9	AV554326
35	123	8.5	527	9	AV553948
36	123	8.5	546	9	AV518519
37	123	8.5	551	9	AV552230
38	120.6	8.4	251	14	CB258935
39	119.8	8.3	270	9	AV519680
40	119	8.2	491	14	T76037
41	119	8.2	502	14	N37237
42	118	8.2	311	14	T20714
43	118	8.2	478	14	R30501
44	116.2	8.0	293	9	AV528010
45	114.8	8.0	821	14	CF651397
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ALIGNMENTS

RESULT 1	BX531590/c	552 bp	DNA	linear	GSS 03-JUN-2003
LOCUS	Arabidopsis thaliana T-DNA flanking sequence GK-481G03-019880,				
DEFINITION	Arabidopsis thaliana T-DNA flanking sequence GK-481G03-019880,				
ACCESSION	BX531590				
VERSION	BX531590.1				
KEYWORDS	GSS.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi				
REFERENCE	1				
AUTHORS	Srithov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. and Weisshaar,B.				
TITLE	A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines				
JOURNAL	Unpublished				
REFERENCE	2				
AUTHORS	Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.				
TITLE	A new Arabidopsis thaliana T-DNA mutagenised population (GABI-kat) for flanking sequence tag based reverse genetics				
JOURNAL	Unpublished				
REFERENCE	3				
AUTHORS	Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B.				

TITLE Direct Submission
JOURNAL Submitted (02-JUN-2003) Weishaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g18780. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES Location/Qualifiers
 1..552
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-481G03-019880"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

ORIGIN
 Query Match 18.9%; Score 272.8; DB 29; Length 552;
 Best Local Similarity 93.9%; Pred. No. 4.3e-50;
 Matches 294; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 1126 GATCCATGTTTCATGTTTACCTGGGAATGATTTGTATGTGAATTTGAAATCTGAACCTTT 1185
 DB 552 GATCCATGTTTCATGTTTACCTGGGAATGATTTGTATGTGAATTTGAAATCTGAACCTTT 493
 QY 1186 GAAGTTAGATTGAATCTGAACCTGTCATGTTAGATTGAATCTGAACCTGTTTAA 1244
 DB 492 GAAGTTAGATTGAATCTGAACCTGTCATGTTAGATTGAATCTGAACCTGTTTAA 433
 QY 1245 TAGATGAAGTTTCTGTATAGATTCTTCGAAACCTTAGATTGTAGTGTGCTGACGTTGAA 1304
 DB 432 TAGATGAAGTTTCTGTATAGATTCTTCGAAACCTTAGATTGTAGTGTGCTGACGTTGAA 373
 QY 1305 CAGAAAGCTATTTTCTGATTAATCAGGGTTTATTTGACTGTATTGAACCTTTTGTGTG 1364
 DB 372 CAGAAAGCTATTTTCTGATTAATCAGGGTTTATTTGCTGTATTGAACCTTTTGTGTG 313
 QY 1365 TTTCGAGCTCATAAAAATGCTGAGGCTGACGATTTTCACCAATCGTGTGACAAATG 1424
 DB 312 TTTCGAGCTCATAAAAATGCTGAGGCTGATGATTTACCCAAATCGTGTGACAAATG 253
 QY 1425 GTACTGGAATGGT 1437
 DB 252 GTACCGGTATGGT 240

RESULT 2
LOCUS AV831431
DEFINITION AV831431 RAF19 Arabidopsis thaliana cDNA clone RAF109-89-B08 5', mRNA sequence.
ACCESSION AV831431
VERSION AV831431.1 GI:19873491
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 327)
AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.

Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y., and Shinozaki, K.
 Large scale analysis of Arabidopsis full-length cDNA (2002b)
 Unpublished (2002)
 Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: maeiki@rken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified lambdaBda F1C-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES Location/Qualifiers
 1..327
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAF109-89-B08"
 /dev_stage="plants at various developmental stages from germination to mature seeds"
 /clone_lib="RAFL9"
 /lab_host="DH10B"
 /notes="Site 1: BamHI; Site 2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"

ORIGIN
 Query Match 14.0%; Score 202.4; DB 9; Length 327;
 Best Local Similarity 94.1%; Pred. No. 1.9e-34;
 Matches 222; Conservative 0; Mismatches 11; Indels 3; Gaps 1;

QY 716 AAACCCGCTATTAATTCATATATTTCTCCCGCTTTGAATTTCTCGTCTGCTC 775
 DB 3 AAACCCGCTATTAATTCATATATTTCTCCCGCTTTGAATTTCTCGTCTGCTC 62
 QY 776 CTCATCTTCATCAGCGTTTGAATCTCCGCGACTTCACAGAGAACAAGGAAG 835
 DB 63 CTCATCTTCATCAGCGTTTGAATCTCCGCGACTTCACAGAGAACAAGGAAG 122
 QY 836 ACTAAGAGAGAAAGTAAGAGATAATCCAGAGATTCATCTCCGTTTGAATCTTCCTCA 895
 DB 123 ACTAAGAGAGAAAGTAAGAGATAATCCAGAGATTCATCTCCGTTTGAATCTTCCTCA 182
 QY 896 ATCTCATCTTCTTCCGCTCTTTCTTCCAGGTAATAGAACTTCTGGATCT 951
 DB 183 ATCTCA---TCTTCTTCCGCTCTTTCTTCCAGGTCATATAAATGGCTGAGGCT 235

RESULT 3
LOCUS AV831862
DEFINITION AV831862 RAF19 Arabidopsis thaliana cDNA clone RAF109-96-J07 5', mRNA sequence.
ACCESSION AV831862
VERSION AV831862.1 GI:19873922
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 600)
AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y., and Shinozaki, K.

Buxaryota, viridiplantae, Scirepophyta, amozyophyta, tracheophyta,
 Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
 rosoids, eurosids II, Brassicales, Brassicaceae, Arabidopsids.
 1 (bases 1 to 396)
 Sasaki, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.,
 and Shinozaki, K.
 Large scale analysis of Arabidopsis full-length cDNA (2002b)
 Unpublished (2002)
 Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: msek@rtc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
 and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
 al., submitted for publication) digested with BamHI and SalI. This
 clone is in a modified Bluescript vector. Please visit our web

site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

source Location/Qualifiers
 1..396
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAFL09-24-N21"
 /dev_stage="plants at various developmental stages from germination to mature seeds"
 /lab_host="DH10B"
 /clone_lib="RAFL9"
 /note="Site 1: BamHI; Site 2: SalI; subjected to denaturation (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"

ORIGIN

Query Match 10.9%; Score 158; DB 9; Length 396;
 Best Local Similarity 93.2%; Pred. No. 1.3e-24;
 Matches 177; Conservative 0; Mismatches 10; Indels 3; Gaps 1;
 762 GTCTCGTTCCTCTCACTTTCATCAGCGGTTTGAATCTCGGCGACTTGACAGAA 821
 Db 2 GTCTCGTTCCTCTCACTTTCATCAGCGGTTTGAATCTCGGCGACTTGACAGAA 61
 822 GAACAGGAGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCTTCGTT 881
 Db 62 GAACAGGAGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCTTCGTT 121
 882 TTGAATCTTCCTCAATCTCATCTTCTTCGCTCTTTCTTCCAAAGTAATAGGAAT 941
 Db 122 TTGAATCTTCCTCAATCTCA---TCTTCTCGCTCTTTCTTCCAAAGTCATAAAAT 178
 942 TTCTGGATCT 951
 Db 179 GGCTGAGGCT 188

RESULT 6

AV830541 562 bp mRNA linear EST 01-APR-2002
 LOCUS AV830541 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-70-008 5',
 DEFINITION mRNA sequence.
 ACCESSION AV830541 GI:19872601
 VERSION AV830541.1
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 562)
 AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
 and Shinozaki, K.
 TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: meeki@rtc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
 and XhoI was ligated to modified Lambda FIC-1 vector (Carninci et
 al., submitted for publication) digested with BamHI and SalI. This
 clone is in a modified pBluescript vector. Please visit our web
 site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

Location/Qualifiers

source

1..562
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAFL09-70-008"
 /dev_stage="plants at various developmental stages from germination to mature seeds"
 /lab_host="DH10B"
 /clone_lib="RAFL9"
 /note="Site 1: BamHI; Site 2: SalI; subjected to denaturation (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"

ORIGIN

Query Match 10.9%; Score 158; DB 9; Length 562;
 Best Local Similarity 93.2%; Pred. No. 1.3e-24;
 Matches 177; Conservative 0; Mismatches 10; Indels 3; Gaps 1;
 762 GTCTCGTTCCTCTCACTTTCATCAGCGGTTTGAATCTCGGCGACTTGACAGAA 821
 Db 2 GTCTCGTTCCTCTCACTTTCATCAGCGGTTTGAATCTCGGCGACTTGACAGAA 61
 822 GAACAGGAGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCTTCGTT 881
 Db 62 GAACAGGAGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCTTCGTT 121
 882 TTGAATCTTCCTCAATCTCATCTTCTTCGCTCTTTCTTCCAAAGTAATAGGAAT 941
 Db 122 TTGAATCTTCCTCAATCTCA---TCTTCTCGCTCTTTCTTCCAAAGTCATAAAAT 178
 942 TTCTGGATCT 951
 Db 179 GGCTGAGGCT 188

RESULT 7

AV831261 580 bp mRNA linear EST 01-APR-2002
 LOCUS AV831261 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-87-G17 5',
 DEFINITION mRNA sequence.
 ACCESSION AV831261 GI:19873321
 VERSION AV831261.1
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 580)
 AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
 and Shinozaki, K.
 TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: meeki@rtc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
 and XhoI was ligated to modified Lambda FIC-1 vector (Carninci et
 al., submitted for publication) digested with BamHI and SalI. This
 clone is in a modified pBluescript vector. Please visit our web
 site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

Location/Qualifiers
 1..580
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"

/db_xref="taxon:3702"
 /clone="RAFL09-87-G17"
 /dev_stage="plants at various developmental stages from germination to mature seeds"
 /lab_host="DH10B"
 /clone_lib="RAFL9"
 /note="Site 1: BamHI; Site 2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"

ORIGIN

Query Match 10.9%; Score 158; DB 9; Length 580;
 Best Local Similarity 93.2%; Pred. No. 1.3e-24;
 Matches 177; Conservative 0; Mismatches 10; Indels 3; Gaps 1;
 QY 762 GTCTGTTGTCCTCTCACTTTCATCAGCCGTTTGAATCTCCGGGACCTTACAGAGAA 821
 Db 1 GTCTGTTGTCCTCTCACTTTCATCAGCCGTTTGAATCTCCGGGACCTTACAGAGAA 60
 QY 822 GAACAGGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGAGATTCATTCCTCGTT 881
 Db 61 GAACAGGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGAGATTCATTCCTCGTT 120
 QY 882 TTGAATCTTCTCAATCTCATCTTCTTCCTCCGCTCTTTTCCAGGTAAATAGAACT 941
 Db 121 TTGAATCTTCTCAATCTCA--TCTTCTCCGCTCTTTTCCAGGTCAFAAAAAAT 177
 QY 942 TTCTGGATCT 951
 Db 178 GGCTGAGGCT 187

RESULT 8
 AV824265
 LOCUS AV824265 RAF16 Arabidopsis thaliana cDNA clone RAFL06-16-M11 5', mRNA sequence.
 DEFINITION AV824265.1 GI:19866325
 ACCESSION AV824265
 VERSION AV824265.1
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 REFERENCE 1 (bases 1 to 667)
 AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
 TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: mseki@rtc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SstI/XhoI insert. Please visit our web site http://www.gsc.riken.go.jp/e/plant/index_e.html for further details.

FEATURES

Location/Qualifiers
 1..667
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAFL06-16-M11"
 /dev_stage="plants at various developmental stages from germination to mature seeds"
 /lab_host="DH10B"

/clone_lib="RAFL6"
 /note="Site 1: SstI; Site 2: XhoI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"

ORIGIN

Query Match 10.9%; Score 158; DB 9; Length 667;
 Best Local Similarity 93.2%; Pred. No. 1.2e-24;
 Matches 177; Conservative 0; Mismatches 10; Indels 3; Gaps 1;
 QY 762 GTCTGTTGTCCTCTCACTTTCATCAGCCGTTTGAATCTCCGGGACCTTACAGAGAA 821
 Db 2 GTCTGTTGTCCTCTCACTTTCATCAGCCGTTTGAATCTCCGGGACCTTACAGAGAA 61
 QY 822 GAACAGGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGAGATTCATTCCTCGTT 881
 Db 62 GAACAGGAGAGACTAAGAGAGAAAGTAAGAGATAATCCAGAGATTCATTCCTCGTT 121
 QY 882 TTGAATCTTCTCAATCTCATCTTCTTCCTCCGCTCTTTTCCAGGTAAATAGAACT 941
 Db 122 TTGAATCTTCTCAATCTCA--TCTTCTCCGCTCTTTTCCAGGTCAFAAAAAAT 178
 QY 942 TTCTGGATCT 951
 Db 179 GGCTGAGGCT 188

RESULT 9
 AV526249
 LOCUS AV526249 538 bp mRNA linear EST 01-SEP-2000
 DEFINITION AV526249 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana cDNA clone APZ08b09R 5', mRNA sequence.
 ACCESSION AV526249
 VERSION AV526249.1
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 REFERENCE 1 (bases 1 to 538)
 AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
 JOURNAL DNA Res. 7 (3), 175-180 (2000)
 MEDLINE 20363093
 PUBMED 10907847
 COMMENT Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp; URL: <http://www.kazusa.or.jp/en/plant/>.
 Location/Qualifiers
 1..538
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="APZ08b09R"
 /tissue_type="aboveground organs"
 /dev_stage="two to six-week old"
 /clone_lib="Arabidopsis thaliana aboveground organs two to six-week old"
 /note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

FEATURES

source
 1..538
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="APZ08b09R"
 /tissue_type="aboveground organs"
 /dev_stage="two to six-week old"
 /clone_lib="Arabidopsis thaliana aboveground organs two to six-week old"
 /note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 10.8%; Score 156; DB 9; Length 538;
 Best Local Similarity 93.1%; Pred. No. 3.5e-24;
 Matches 175; Conservative 0; Mismatches 10; Indels 3; Gaps 1;
 QY 764 CTGCTGTCTCTCACTTTCATCAGCCGTTTGAATCTCCGGGACCTTACAGAGAA 823

Db 1 CTGTTGTCCTCTCACTTTTCATCAGCGTTTGAATCTCCGCGACTTGACAGAGA 60
 QY 824 ACAGAGAGAGAGACTTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTCTCCGTTT 883
 Db 61 ACAGAGAGAGAGACTTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTCTCCGTTT 120
 QY 884 GAATCTCTCAATCTCACTTTCTTCTCCGCTCTTTTCCAGGTAATAGGACTTTT 943
 Db 121 GAATCTCTCAATCTCACTTTCTTCTCCGCTCTTTTCCAGGTAATAGGACTTTT 177
 QY 944 CTGAGTCT 951
 Db 178 CTGAGGCT 185

RESULT 10
 AV829675 399 bp mRNA linear EST 01-APR-2002
 LOCUS AV829675 RAPL9 Arabidopsis thaliana CDNA clone RAPL09-49-P05 5',
 DEFINITION mRNA sequence.

ACCESSION AV829675.1 GI:19871735
 VERSION AV829675
 KEYWORDS EST
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 399)
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 399)
 AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
 and Shinozaki, K.

TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Motoaki Seki

Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060

Email: meeki@rc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
 and XhoI was ligated to modified Lambda fuc-1 vector (Carninci et
 al., submitted for publication) digested with BamHI and SalI. This
 clone is in a modified pBluescript vector. Please visit our web
 site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
 details.

FEATURES
 source
 1..399
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAPL09-49-P05"
 /dev_stage="plants at various developmental stages from
 germination to mature seeds"
 /lab_host="DH10B"
 /clone_lib="RAPL9"
 /notes="Site 1: BamHI; Site 2: SalI; subjected to
 dehydration (1, 2, 5, 10, 24 hr) treatments"

ORIGIN
 Query Match 10.6%; Score 153; DB 9; Length 399;
 Best Local Similarity 93.0%; Pred. No. 1.7e-23;
 Matches 172; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

QY 767 GTTGTCCTCTCACTTTTCATCAGCGTTTGAATCTCCGCGACTTGACAGAGAGA 826
 Db 2 GTTGTCCTCTCACTTTTCATCAGCGTTTGAATCTCCGCGACTTGACAGAGAGA 61

QY 827 AGGAGAGAGACTTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTCTCGTTTGA 886
 Db 62 AGGAGAGAGACTTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTCTCGTTTGA 121
 QY 887 TCTTCTCTCAATCTCACTTTCTTCTCCGCTCTTTTCCAGGTAATAGGACTTTCTG 946
 Db 122 TCTTCTCTCAATCTCACTTTCTTCTCCGCTCTTTTCCAGGTAATAGGACTTTG 178
 QY 947 GATCT 951
 Db 179 AGGCT 183

RESULT 11
 AV525898 297 bp mRNA linear EST 01-SEP-2000
 LOCUS AV525898 Arabidopsis thaliana aboveground organs two to six-week
 DEFINITION old Arabidopsis thaliana CDNA clone APD32B06R 5', mRNA sequence.

ACCESSION AV525898.1 GI:8685426
 VERSION AV525898
 KEYWORDS EST
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 297)
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 297)
 AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
 of 12,028 non-redundant expressed sequence tags from normalized and
 size-selected cDNA libraries
 JOURNAL DNA Res. 7 (3), 175-180 (2000)
 MEDLINE 20363093
 PUBMED 10907847

COMMENT Contact: Erika Asamizu
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 Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES
 source
 1..297
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="APD32B06R"
 /tissue_type="aboveground organs"
 /dev_stage="two to six-week old"
 /clone_lib="Arabidopsis thaliana aboveground organs two to
 six-week old"
 /notes="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 XhoI"

ORIGIN
 Query Match 10.5%; Score 151; DB 9; Length 297;
 Best Local Similarity 92.9%; Pred. No. 4.8e-23;
 Matches 170; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

QY 769 TGTCTCTCTCACTTTTCATCAGCGCTTTTGAATCTCCGCGACTTGACAGAGAGACA 828
 Db 1 TGTCTCTCTCACTTTTCATCAGCGCTTTTGAATCTCCGCGACTTGACAGAGAGACA 60

QY 829 GAAGAGAGACTTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTCTCGTTTGA 889
 Db 61 GAAGAGAGACTTAAGAGAGAAAGTAAGAGATAATCCAGGAGATTCATTCTCGTTTGA 120

QY 889 TTTCTCAATCTCACTTTCTTCTTCTCCGCTCTTTTCCAGGTAATAGGACTTTCTGA 948
 Db 121 TTTCTCAATCTCACTTTCTTCTTCTCCGCTCTTTTCCAGGTAATAGGACTTTCTGA 177
 QY 949 TCT 951
 Db 178 GCT 180

RESULT 12
BH901724/c
LOCUS
DEFINITION
 BH901724 162 bp DNA linear GSS 04-SEP-2002
 SALK 085874.51.15.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_085874.51.15.x, genomic
 survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 Arabidopsis thaliana (thale cress)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
 1 (bases 1 to 162)

REFERENCE
AUTHORS
 Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jester, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shin, P., Zimmerman, J. and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.

FEATURES
 Class: TDNA tagged.
 Location/Qualifiers
 1..162
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_085874.51.15.x"
 /notes="PCR was performed on Arabidopsis thaliana TDNA insertion lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
 Query Match 10.4%; Score 150; DB 28; Length 162;
 Best Local Similarity 99.4%; Pred. No. 8.6e-23;
 Matches 161; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 575 TAATTAGTTTAAATAATAGTTTAAACAGAGGAGAAA-GCTGTCTGACAGCCAGGTACAGTT 633
 Db 162 TAATTAGTTTAAATAATAGTTTAAACAGAGGAGAGGCTGTCTGACAGCCAGGTACAGTT 103
 QY 634 ATCTTTACCTGTGCTGGAATGATCGTGTCTGATGATTTAATTAATTTTGAAGGC 693
 Db 102 ATCTTTACCTGTGCTGGAATGATCGTGTCTGATGATTTAATTAATTTTGAAGGC 43
 QY 694 CGAATAATAGTTTGAAGAGATAACCCGCTATATAATTC 735
 Db 42 CGAATAATAGTTTGAAGAGATAACCCGCTATATAATTC 1

RESULT 13
BU635286
LOCUS
DEFINITION
 BU635286 774 bp mRNA linear EST 23-SEP-2002
 018F03 Infected Arabidopsis Leaf Arabidopsis thaliana cDNA, mRNA
 sequence.

ACCESSION
VERSION
 BU635286.1 GI:23302541

KEYWORDS
SOURCE
ORGANISM
 Arabidopsis thaliana (thale cress)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
 1 (bases 1 to 774)

REFERENCE
AUTHORS
 Lundsgaard, M., Emmersen, J., Nielsen, K.L., Wilson, J., Somerville, S.
 and Welinder, K.G.
 EST sequencing of Erysiphe cichoracearum infected Arabidopsis
 plants
 Unpublished (2002)
 Contact: Karen G. Welinder
 Institut for bioteknologi
 Aalborg Universitet
 Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
 Tel: +45 96358467
 Fax: +45 98141808
 Email: kgw@bio.auc.dk
 Location/Qualifiers
 1..774
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /dev_stage="Plant 3 weeks old, three days post infection"
 /clone_lib="Infected Arabidopsis Leaf"
 /notes="Organ: Leaf; Vector: pBluescript; Mixed cDNA
 library of Arabidopsis and E. cichoracearum infected leaf
 from three weeks old Arabidopsis plants. Plants were
 harvested 3 days after infection and mRNA oligo dT
 selected."

FEATURES
 source

ORIGIN
 Query Match 10.2%; Score 147; DB 13; Length 774;
 Best Local Similarity 92.7%; Pred. No. 3.4e-22;
 Matches 166; Conservative 0; Mismatches 10; Indels 3; Gaps 1;
 QY 773 CTCCTCACTTTCATCAGCCGTTTGAATCTCCGGGACTTCACAGAGAACACAGGAG 832
 Db 15 CTCCTCACTTTCATCAGCCGTTTGAATCTCCGGGACTTCACAGAGAACACAGGAG 74
 QY 833 AGACATAGAGAGAAAGTAAGAGATAATCCAGAGATTCATTCTCCGTTTGAATCTTCC 892
 Db 75 AGACATAGAGAGAAAGTAAGAGATAATCCAGAGATTCATTCTCCGTTTGAATCTTCC 134
 QY 893 TCAATCTCATCTTCTTCTTCCGCTCTTCTTCCAGAGTAATAGGAACATTTCTGATCT 951
 Db 135 TCAATCTCA---TCTTCTTCGCTCTTCTTCCAGGCTCATATAAATAATGGCTGAGGCT 190

RESULT 14
N65062
LOCUS
DEFINITION
 N65062 463 bp mRNA linear EST 05-JAN-1998
 20102 Lambda-PRL2 Arabidopsis thaliana cDNA clone 226A8T7, mRNA
 sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 Arabidopsis thaliana (thale cress)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
 1 (bases 1 to 463)

REFERENCE
AUTHORS
 Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,
 McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomasow, M.,
 Retzel, E. and Somerville, C.
 Genes galore: a summary of methods for accessing results from
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones
 Plant Physiol. 106, 1241-1255 (1994)

JOURNAL
MEDLINE
PUBMED
 7846151

COMMENT

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Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.

FEATURES

source

Location/Qualifiers

1..463
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="var columbia"
/db_xref="taxon:3702"
/clone="226A8T7"
/clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site 1: Sal; Site 2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
silicles). The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dt primed cDNA. "

ORIGIN

Query Match 10.1%; Score 146; DB 14; Length 463;
Best local similarity 92.7%; Pred. No. 6e-22; Indels 3; Gaps 1;
Matches 165; Conservative 0; Mismatches 10;
QY 774 TCCTCATTTCATCAGCGCTTTGAATCTCCGGCAGCTTGACAGAGAAGAACAGGAAGA 833
Db 1 TCCTCATTTCATCAGCGCTTTGAATCTCCGGCAGCTTGACAGAGAAGAACAGGAAGA 60
QY 834 AGACTAAGAGAGAAGTAAGAGATAATCCAGGAGATTCATTCTCGTTTGAATCTTCT 893
Db 61 AGACTAAGAGAGAAGTAAGAGATAATCCAGGAGATTCATTCTCGTTTGAATCTTCT 120
QY 894 CAATCTCATCTTCTTCTCGCTCTTTCTTTCCAGGTAATAGGAACCTTCTCGATCT 951
Db 121 CAATCTCA---TCTTCTCGCTCTTCTTTCCAGCTCATTAATAATGCTGAGGCT 175

RESULT 15

N38049
LOCUS N38049 438 bp mRNA linear EST 05-JAN-1998
DEFINITION 13276 Lambda-PRL2 Arabidopsis thaliana cDNA clone 217C7T7, mRNA
sequence.

ACCESSION

N38049

VERSION

N38049.1 GI:1159191

KEYWORDS

EST.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 438)

Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,

McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,

Retzel, E. and Somerville, C.

Genes galore: a summary of methods for accessing results from

large-scale partial sequencing of anonymous Arabidopsis cDNA clones

Plant Physiol. 106, 1241-1255 (1994)

95148729

7846151

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Email: 22313tcn@ibm.cl.msu.edu

Seq primer: T7 dye primer.

FEATURES

source

Location/Qualifiers

1..438
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="var columbia"
/db_xref="taxon:3702"
/clone="217C7T7"
/clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site 1: Sal; Site 2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
silicles). The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dt primed cDNA. "

ORIGIN

Query Match 10.0%; Score 144; DB 14; Length 438;
Best local similarity 92.6%; Pred. No. 1.7e-21; Indels 3; Gaps 1;
Matches 163; Conservative 0; Mismatches 10;
QY 776 CTCACCTTTCATCAGCGCTTTGAATCTCCGGCAGCTTGACAGAGAAGAACAGGAAGAAG 835
Db 1 CTCACCTTTCATCAGCGCTTTGAATCTCCGGCAGCTTGACAGAGAAGAACAGGAAGAAG 60
QY 836 ACTAAGAGAGAAGTAAGAGATAATCCAGGAGATTCATTCTCGTTTGAATCTTCTCTCA 895
Db 61 ACTAAGAGAGAAGTAAGAGATAATCCAGGAGATTCATTCTCGTTTGAATCTTCTCTCA 120
QY 896 ATCTCATCTTCTTCTCGCTCTTTCTTTCCAGGTAATAGGAACCTTCTCGATCT 951
Db 121 ATCTCA---TCTTCTCGCTCTTCTTTCCAGCTCATTAATAATGCTGAGGCT 173

Search completed: March 15, 2004, 01:43:50

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